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14. ABSTRACT
The intent of this project was to integrate whole exome genetic and global expression data to identify genes that contribute to the formation, progression and heterogeneity of NF2-associated tumors. We first prepared and submitted for exome sequencing 126 samples representing paired human tumor (meningioma or schwannoma) and normal DNAs from the same individuals. We also prepared RNA from the same tumors for transcriptome sequencing. We then complemented these datasets with RNA expression data from of a panel of isogenic arachnoidal cell lines either heterozygous or homozygous for inactivating *NF2* mutation to define the primary effects of merlin loss in this cell type, which gives rise to meningiomas. Our analyses indicate that secondary mutations in meningiomas occur primarily as large chromosomal structural variations rather than point mutations, in contrast with schwannomas where tentative second-hit somatic alteration of particular genes was noted. Our expression studies also implicate several genes as potential targets for therapeutic approaches for meningioma.

15. SUBJECT TERMS
Neurofibromatosis 2, meningioma, schwannoma, exome, transcriptome

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Introduction

In neurofibromatosis 2 (NF2), tumor formation requires inheritance of a germline mutation in the *NF2* gene that inactivates one allelic dose of the merlin tumor suppressor, followed by somatic loss or inactivation of the remaining allele. However, it is not known whether merlin deficiency alone is sufficient for tumor formation, either in schwannomas or in meningiomas, the two major tumor types of NF2. A number of lines of evidence suggest that other genetic lesions may participate in the initiation of NF2 tumors and that other genes certainly contribute to the functional heterogeneity and progression observed in meningiomas. In the latter instance, there are many studies that have noted rearrangements of particular chromosomal regions in merlin-deficient meningiomas, but despite many years of investigation of these regions, the critical genes that participate in tumor development and heterogeneity and the biological pathways that they represent remain unknown. We postulated that there are somatic genetic events that occur in individual genes that contribute to the formation, progression and heterogeneity of tumors in NF2 and that integrated analysis of whole exome sequence data together with tumor characteristics, genomic rearrangements, and RNA expression data from these tumors in comparison with normal arachnoidal cells would reveal the biological pathways that underlie the development and functional heterogeneity of NF2 meningiomas.

Keywords

Neurofibromatosis 2, meningioma, schwannoma, exome, transcriptome, arachnoid, CRISPR

Overall Project Summary

Task 1- DNA sequence analysis of meningiomas

Our first specific aim was to perform paired whole exome sequencing of meningiomas and normal DNAs from the same individuals to identify *de novo*, somatic alterations, from point mutations and small insertion/deletions that affect protein structure to large regions of loss-of-heterozygosity (LOH). We also indicated the possibility of complementing these analyses of meningioma with similar analyses of the other NF2-associated tumor, schwannoma. The goal in Year 1 was to generate exome data from the first 30 of these meningiomas and their matching normal DNAs. We first successfully screened a large number of tumors and selected those for exome sequencing. We then generated high quality DNA from 26 meningiomas (4 sporadic and 22 NF2-associated) with matched blood DNA. We also augmented this analysis by preparing high quality DNA from 30 vestibular schwannomas (4 NF2 and 26 sporadic) all obtained through clinically-indicated surgery and their corresponding blood DNA. In addition, we prepared DNA from 8 meningiomas, 5 vestibular schwannomas, 4 nerve samples and 1 arachnoid sample from two independent NF2 autopsies. We then submitted DNA from 126 samples (63 tumor and normal DNA pairs) to the DNA Sequencing Facility for preparation of exome capture libraries, indexing and deep sequencing using Illumina HiSeq2500 DNA Analyzers. By running this larger than anticipated number of tumors in a single batch, we avoided the potential batch effects of splitting the analysis into two batches of ~60.

In Year 2, we received and analyzed the exome data from these tumors. The exome sequences were generated by Illumina 76 paired-end sequence reads at the Broad Institute Genome Analysis Platform. Sequence reads that were demultiplexed by Illumina's CASAVA software, were mapped to the human genome build 37 (hg19) through BWA v. 0.5.9 [1] with parameters -q 5 -l 32 -k 2 –o 1. The resulting alignments were further sorted, indexed and duplicates removed using the Picard Tools [http://broadinstitute.github.io/picard/]. Next, base quality score recalibration and local realignment around known indels were performed using GATK [2,3]. In this process, five meningioma and two schwannoma samples failed to pass the QC metrics and thus, they were removed from more detailed analysis.

Somatic variants were called applying muTect v.1.1.4 [4] with parameters –min_qscore 20 –clipping_bias_pvalue_threshold 0.05 and Indelocator [https://www.broadinstitute.org/cancer/cga/indelocator] with a parameter –ws 300 to blood-matched tumor pairs to identify single nucleotide variants and small indels respectively. Variants were identified only in the target exon intervals used in the exome capture sequencing. Next, identified variants with the respective read depths ≥8X and ≥14X in paired blood and tumor samples, and tumor fraction ≥ 0.1 were annotated using Oncotator v.1.3 [5] with the oncotator_v1_ds_Sept172014 database.

Additionally, alignability scores (≥ 0.8) based on alignability of 36mers [6] were applied to further filter the variants.

For defining candidate genes whose inactivation contributes to tumorigenesis, we identified all *de novo* somatic variants in the exome data and classified them into loss-of-function mutations (nonsense, frame shift deletion and insertion, and splice_site), missense mutations with deleterious effect predicted by PolyPhen [7], Sift[8], Mutation Assessor [9], Mutation Taster[10] and LRT [11], and other non-synonymous mutations such as in_frame indels, and enforcing ≥10X coverage in blood samples. Overall, the raw calls from muTect and Indelicator indicated 1,481 *de novo* somatic sequence variants called in the exon and immediately adjacent intron regions in primary meningioma samples relative to the constitutional DNA from the same individual. Less than 10% of these were predicted to have a clear deleterious effect on the protein encoded by the corresponding gene (19 nonsense, 13 splice site, 56 frameshift, 2 start codon mutation). Among the schwannomas, 2,374 *de novo* sequence variants were called, including 22 nonsense mutations, 25 splice site, 66 frameshifts, and 20 in-frame indels. The variant-called reads were often present at significantly less than 50% of all reads, suggesting that there was mosaicism within some tumors. As expected. the *NF2* gene showed evident inactivating *de novo* somatic mutations with 4 nonsense changes in meningiomas and 3 nonsense, 8 frameshift and 5 splice site changes in schwannomas.

After filtering out sites where the total read count was <10, requiring stringent read quality scores and assessing missense mutations for their likelihood of having deleterious effects, a small subset of genes each appeared to display two independent somatic hits across these tumors, making these loci candidates for further analysis. These variants are shown in Table 1, with the gene name, function, location and size, accompanied by the specific nature of the sequence variation and what proportion of reads in the exome data revealed the alternate sequence. These genes were mutated primarily in schwannomas rather than in meningiomas, which, along with the difference in the frequency of dosage change (see below), suggested a somewhat different genetic architecture in these two tumor types, with the exception of chromosome 22 loss (the site of the *NF2* gene) which occurs at very high frequency in both.

Table 1- Candidate contributors to tumorigenesis based upon recurrent mutation

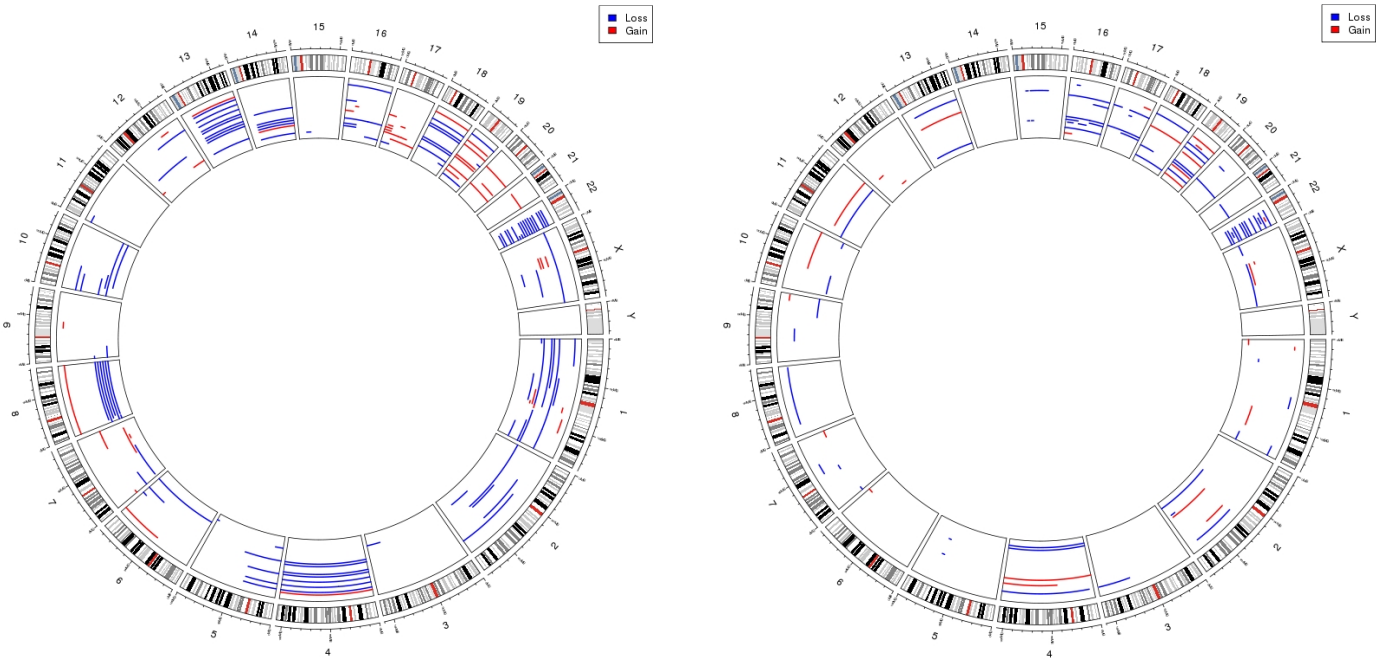
Schwannoma									
Gene Name	**Function**	**Location**	**# Exons**	**Total gene size (bp)**	**Transcript change**	**Protein change**	**# Reads of somatic variant/ total reads**	**# Tumors**	**# Confirmed by resequencing**
PAK2	p21-activated kinase (cytoskeletal)	3:196466728 - 196559518	15	92791	c.1493C>T, c.383A>G	p.P498L, p.K128R	4/24; 9/36	2	0
PRDM1	Represses beta-interferon expression	6:106534195 - 106557814	7	23620	c.2119G>A, c.202delA	p.E707K, p.K68fs	8/54; 12/30	2	2
NUP153	Nuclear pore complex	6:17615266-17707065	22	91800	c.1633A>G, c.3897_3899delTGC	p.I545V, p.A1300del	10/18; 7/19	2	1
RYR2	Ryanodine receptor	1:237205702 - 237997288	105	791587	c.2080C>T, c.10820_10821insT	p.R694*, p.PL3607fs	8/53; 5/16	2	1
UNC5A	Netrin receptor (axonal migration)	5:176237560 - 176307899	15	70340	c.1103C>T, c.1220G>A	p.P368L, p.R407H	10/15; 5/25	2	2
ZCCHC14	Zinc finger, phosphatidylinositol binding	16:87439852 - 87525460	13	85609	c.25A>T, c.17C<G	p.S9C, p.P6R	4/15; 4/19	2	2 (both proved to be germline)
Meningioma									
NLRP1	Ced-4 family of apoptosis proteins	17:5404719-5487832	16	83114	c.1853delG, c.916G>C	p.S618fs, p.E306Q	22/48; 6/17	2	1

We initially attempted to validate the presence of each of these mutations in the corresponding tumor and its absence in the blood DNA using Sanger sequencing of specific PCR products. The results were disappointing, as many variants were not easily seen in the Sanger sequencing. Consequently, we turned to MiSeq targeted

next generation sequencing in an attempt to verify each of these 14 putative somatic mutations. In all, 7 of the 14 candidate variants (those shown in red) were confirmed as present in the tumor DNA and also absent in the constitutional DNA. In the case of *ZCCHC14,* both variants were confirmed in tumor DNA but were also found in the constitutional DNA, indicating that they represent germline changes that were missed by the whole exome scan in the analysis of blood DNA. The 5 remaining variants were not seen in the MiSeq sequencing of tumor DNA. The failure to confirm many of these changes could reflect false positives in the original calling of variants in the exome sequencing or more likely mosaicism in the frozen tumor specimens since a new DNA preparation was used for this second stage. The potential for mosaicism in the tumors is supported by the ratio of reads of the *de novo* somatic variant often being far less than 50% of total reads, even for some tumors where the variant was confirmed by resequencing. Among this list of candidate genes, both *UNC5A* and *PRMD1* mutations were confirmed to be present and somatic in origin in both tumors. As a follow up to this analysis, we have now extracted DNA from an additional 47 schwannomas in which we are performing targeted sequencing of *UNC5A* and *PRMD1* exons to look for additional mutations. We will do the same for the remaining 4 genes on the list only if the second unconfirmed mutation in these genes can be verified by further DNA sequencing. If we identify a deleterious somatic mutation in any of the 47 additional tumors, it could confirm *UNC5A* or *PRMD1* as an important candidate for further evaluation of a role in the genesis and growth of schwannomas, since the first two hits came from scanning only 30 schwannomas (7%).

We also performed dosage analysis using the exome read counts to define chromosomal rearrangements in these tumors. First, we computed read depth coverage metrics for target intervals of at least 20 bp in length that were used in the exome sequencing for each sample in the analysis using GATK's DepthOfCoverage walker with –minMappingQuality 20 option [2]. Further, coverage metrics were GC-content normalized as described in [12], where GC-content for target intervals was calculated by GATK's GCContentByInterval walker [2]. Next, log2 ratios of normalized read depth between tumor and matched blood for each target interval with > 5X coverage in both test and control samples were calculated. Log2 ratios were further scaled by subtracting the median of all log2 ratios in the sample. Relying on scaled log2 ratios, we used R's DNAcopy package to segment the data. Later, segments were merged with VarScan's mergesegments.pl script using -0.4 and 0.4 thresholds for deletions and amplifications respectively [13]. Consistent with prior studies from ourselves and others using dosage array analyses, the exome read counts suggested extensive regions of chromosome loss and some regions of duplication. Dosage changes >5Mb usually contained enough exons to be called reliably, and these events were much more prominent in meningiomas than in schwannomas (Figure 1). The meningiomas frequently displayed dosage changes that affected most or all of a chromosome arm, particularly loss events on chromosomes 4, 8,13,14, and 18, and especially on chromosome 22, the site of the *NF2* gene. Such events were less frequent in schwannomas and show a different overall pattern, except for frequent loss of chromosome 22, as expected for a tumor type associated with merlin inactivation.

Figure 1- Dosage alterations by chromosome in meningiomas (left) and schwannomas (right)



Our overall conclusion from this task is that progression of meningiomas occurs predominantly via chromosome rearrangements leading to dosage imbalance rather than through somatic mutation of a limited set of specific progression genes. By contrast, schwannomas show somewhat less dosage imbalance but may harbor specific somatic point mutations in particular genes that contribute to tumor growth. The unequal read counts between mutated and wild-type gene copies suggest that these tumors may be mosaic for the second-hit variations that are detected, indicating that single-cell analysis or *in vitro* modeling studies may be required to fully assess the significance of these somatic events. We are currently preparing a publication that will describe these results, and intend to submit as soon as our follow-up of *UNC5A* and *PRMD1* is completed.

Task 2. RNA and microRNA sequence analysis of meningiomas

Our second specific aim was to perform RNA sequencing (RNA-seq) to define expression profiles relative to normal arachnoid tissue in the same set of meningiomas used for exome analysis above. We performed RNAseq and miRNAseq for 23 primary meningiomas obtained at surgery, 4 meningiomas obtained at autopsy, 4 arachnoid tissue samples obtained at autopsy, a cultured benign meningioma line (BenMen1) [14], a *NF2* heterozygote arachnoidal line (AC7_A3) [15] and 3 *NF2*-null arachnoidal lines isogenic with AC7_A3 except for CRISPR/Cas9 editing of *NF2* (see Table 2).

Table 2 – Isogenic human arachnoidal cell (AC) clones with *NF2* (exon 8) inactivating mutations generated by CRISPR/Cas genome editing

Cell line	clone #	NF2 genotype	merlin expression	NF2 mutations
AC_7	A3	WT/null	yes	Exon 8, wildtype Exon 15, c.1599_1602delGCAT (het)
AC_7	A4	null/null	no	Exon 15, c.1599_1602delGCAT (het) Exon 8, c. 787del23bp (het) Exon 8, c. 804insC (het)
AC_7	A17	null/null	no	Exon 15, c.1599_1602delGCAT (het) Exon 8, c. 795del8bp (het) Exon 8, c. 802insT (het)
AC_7	A19	null/null	no	Exon 15, c.1599_1602delGCAT (het) Exon 8, c. 787del35bp (hom)

RNAseq libraries were prepared using a customized version of a strand-specific dUTP method [16,17]. Libraries were sequenced with 76-bp paired-reads on the Illumina platform. The quality of raw sequence reads were assessed by FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and they were further quality trimmed using sickle with options –q 20 –l 70 [18]. Unfortunately, all autopsy tissues and 1 surgical meningioma specimen yielded libraries that failed quality control metrics, indicating low quality RNA. Consequently these were not analyzed further, but the lack of normal *in vivo* arachnoidal tissue meant the absence in later analyses of a true normal tissue comparison for the meningiomas. Sequences for the remaining 27 libraries were aligned to the human genome (GrCH37, Ensembl build 71) using Gsnap [19] version 2014_12_19. Expression levels of genes in the units of count-per-million were estimated by using bedtools and Ensembl's gene annotation as described in [20] based on uniquely aligned reads. We also prepared and sequenced 36 miRNA libraries 36bp single-end reads on the Illumina platform. The average number of reads per library was 31.7 million and one library failed in sequencing. The raw reads were first trimmed against small-rna sequencing adapters using cutadapt v. with -e 0.1 –O 5 –m 5 options [21]. We next aligned the reads with length between 16 and 25 nt to known mature miRNA sequences from miRBase database [22] (release 21) using BWA aln with –n 1 option [23]. The average number of mapped reads per library was 4.56 million as seven libraries yielded less than two million reads.

As an example of the gene expression data, Figure 2 shows a multi-dimensional scaling plot (equivalent to Principal Components Analysis) comparing gene expression in these samples, revealing close clustering of all 3 CRISPR/Cas9 edited *NF2*-null lines (AC7_A4, AC7_A17, AC7_A19, orange font) and the BenMen1 line

(black font), with clear separation from the wild-type arachnoidal line, AC7_A3 (orange font). There is a clear separation of all of these lines from the meningioma specimens (NF2-derived, purple font; sporadic, green font), reflecting the difference between *in vivo* culture and surgical collection. Also evident is a spread of the primary meningioma samples suggesting greater heterogeneity of expression than among the cultured lines, consistent with the extensive dosage changes seen in Task 1 and the non-isogenic nature of the tumors.

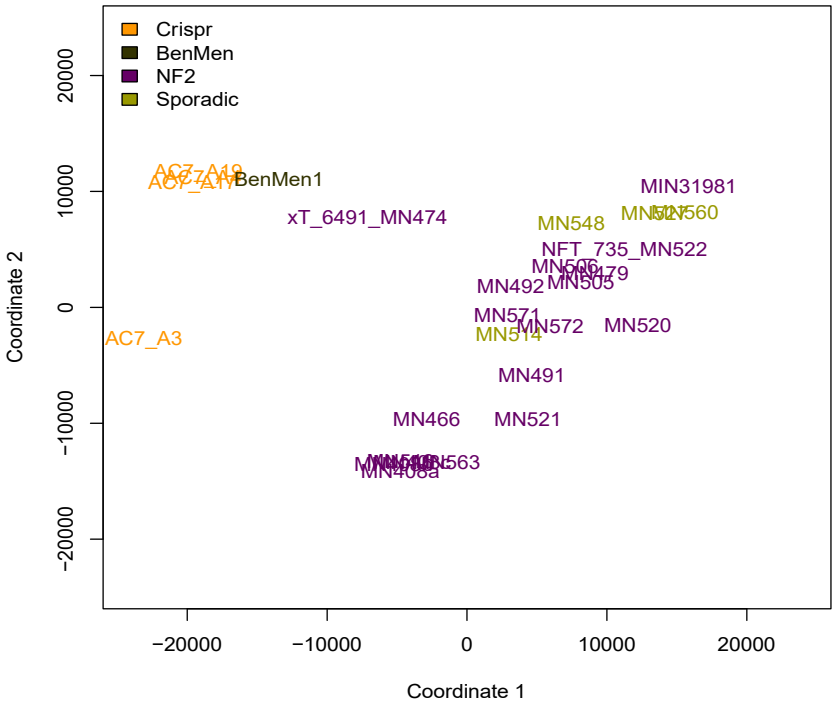


Figure 2- MDS Plot based upon global gene expression

In initial analyses of differential gene expression, we calculated log2 ratios of expression values between test samples and controls and further converted them to Z-scores. After thresholding at > 1 CPM (count per million) in either all treatment samples or in the control sample and A (average log CPM) ≥ -0.5), 13,536 genes were available for comparison of expression. A total of 942 genes (7%) were defined as differentially expressed (abs(M) > log2(1.3) and top 10% z > 11.53): 494 up-regulated and 448 down-regulated by merlin inactivation (a list of these differentially expressed genes is included in the Appendix). Notably, among the top upregulated genes by Z score (2nd on the Appendix list) was *SGK1,* encoding serum/glucocorticoid-regulated kinase 1, which was previously implicated as a potential therapeutic target downstream of MTOR [15].

In the absence of a true tissue control for the primary meningioma specimens (due to the failure of the autopsy tissue specimens to yield high quality RNA libraries), we compared the tumor gene expression to the merlin-expressing arachnoidal cell line, AC7_A3. After thresholding at > 1 CPM in either 12 of the meningiomas or the control sample and A ≥ -0.5, there were 14,641 genes available for comparison. Of these, 1395 genes (9.5%) were differentially expressed (abs(M) > log2(2) and top 10% z > 3.149), 1079 more highly in meningiomas and 316 more highly in the cultured arachnoidal line (the list of these genes is given in the Appendix).

We then performed preliminary GO term and pathway enrichments by DAVID [24] relying on differentially expressed genes identified in the above analyses. The pathways found to be altered by merlin inactivation in the culture cell system are given in Table 3 with the direction of dysregulation of the genes enriched therein, the type and name of the pathway set, along with the number of genes from that set, the P value achieved, the fold enrichment observed and the Benjamini-Hochberg-corrected P value. Shown are all pathway results with a Benjamini P-value <0.1 due to the weak power of this initial analysis. These pathways reflected a variety of cellular functions including a number of terms associated with mitochondria being enriched for upregulated genes. The most statistically significant terms were associated with downregulation of genes involved in cation/metal binding, reflecting in part of a number of zinc finger protein genes whose expression was reduced.

Table 3- Top pathways enriched for genes up- and down-regulated due to merlin loss in initial, limited arachnoidal cell RNA sequencing data

Effect	Category	Term	Count	PValue	Fold Enrichment	Benjamini P value
Upregulated	GOTERM_CC_FAT	GO:0005739~mitochondrion	64	1.00E-05	1.73	3.52E-03
Upregulated	GOTERM_CC_FAT	GO:0044429~mitochondrial part	41	2.94E-05	1.99	5.17E-03
Upregulated	GOTERM_CC_FAT	GO:0005832~chaperonin-containing T-complex	5	9.10E-05	17.21	1.06E-02
Upregulated	BIOCARTA	h_glycolysisPathway:Glycolysis Pathway	5	2.10E-04	13.74	2.33E-02
Upregulated	GOTERM_CC_FAT	GO:0005829~cytosol	67	4.23E-04	1.50	2.93E-02
Upregulated	GOTERM_CC_FAT	GO:0030532~small nuclear ribonucleoprotein complex	7	3.41E-04	7.03	2.96E-02
Upregulated	GOTERM_CC_FAT	GO:0031975~envelope	38	6.20E-04	1.78	3.07E-02
Upregulated	GOTERM_CC_FAT	GO:0031967~organelle envelope	38	5.74E-04	1.78	3.31E-02
Upregulated	GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	28	9.12E-04	1.97	3.93E-02
Upregulated	GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	26	1.70E-03	1.95	6.45E-02
Downregulated	GOTERM_MF_FAT	GO:0043169~cation binding	136	6.14E-07	1.41	9.76E-05
Downregulated	GOTERM_MF_FAT	GO:0043167~ion binding	137	5.78E-07	1.41	1.38E-04
Downregulated	GOTERM_MF_FAT	GO:0046872~metal ion binding	136	3.64E-07	1.42	1.74E-04
Downregulated	GOTERM_MF_FAT	GO:0008270~zinc ion binding	90	1.95E-05	1.50	2.32E-03
Downregulated	GOTERM_MF_FAT	GO:0005509~calcium ion binding	34	2.79E-05	2.19	2.66E-03
Downregulated	GOTERM_MF_FAT	GO:0046914~transition metal ion binding	98	1.47E-04	1.40	1.16E-02
Downregulated	GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	66	2.26E-05	1.66	1.85E-02
Downregulated	GOTERM_BP_FAT	GO:0045449~regulation of transcription	93	1.34E-05	1.50	2.19E-02
Downregulated	GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	66	5.06E-05	1.62	2.75E-02
Downregulated	REACTOME_PATHWAY	REACT_604:Hemostasis	10	1.31E-03	3.51	3.60E-02
Downregulated	GOTERM_CC_FAT	GO:0005886~plasma membrane	69	9.36E-04	1.43	4.86E-02
Downregulated	GOTERM_BP_FAT	GO:0001501~skeletal system development	18	1.25E-04	2.94	5.03E-02
Downregulated	GOTERM_CC_FAT	GO:0031012~extracellular matrix	16	2.01E-04	3.07	5.20E-02
Downregulated	GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	14	8.86E-04	2.94	5.73E-02
Downregulated	GOTERM_CC_FAT	GO:0031983~vesicle lumen	5	3.02E-03	8.00	6.48E-02
Downregulated	GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	27	1.76E-03	1.90	6.49E-02
Downregulated	GOTERM_CC_FAT	GO:0044421~extracellular region part	22	2.95E-03	2.00	6.90E-02
Downregulated	GOTERM_CC_FAT	GO:0031093~platelet alpha granule lumen	5	1.65E-03	9.33	7.07E-02
Downregulated	GOTERM_CC_FAT	GO:0016021~integral to membrane	95	8.66E-04	1.32	7.39E-02
Downregulated	GOTERM_CC_FAT	GO:0009986~cell surface	13	2.89E-03	2.71	7.40E-02
Downregulated	GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	26	2.68E-03	1.87	7.63E-02
Downregulated	GOTERM_CC_FAT	GO:0060205~cytoplasmic membrane-bounded vesicle lumen	5	2.50E-03	8.40	7.98E-02
Downregulated	GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	98	7.27E-04	1.31	9.22E-02
Downregulated	GOTERM_CC_FAT	GO:0031091~platelet alpha granule	5	4.99E-03	7.00	9.74E-02

The pathway analyses of the meningioma samples are given in Tables 4 and 5. Table 4 shows that the genes that are more highly expressed in the primary meningiomas than in the cultured arachnoidal cells are enriched in a variety of pathways associated with the immune system and inflammation. We believe that this may reflect the presence of infiltrating immune system cells within the human tumor specimens.

Table 4- Top pathways enriched for genes more highly expressed in merlin-deficient meningiomas than in the merlin-expressing arachnoidal cell line

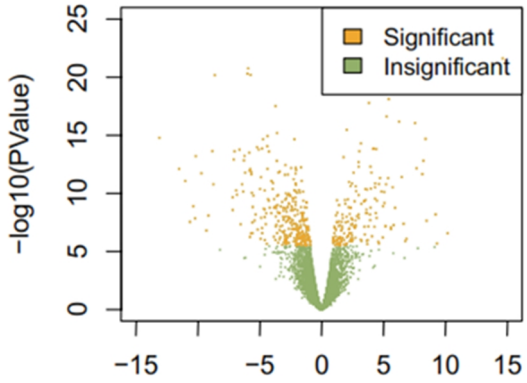
Category	Term	Count	PValue	Fold Enrichment	Benjamini P-value
GOTERM_BP_FAT	GO:0006955~immune response	72	8.91E-19	3.15	2.31E-15
REACTOME_PATHWAY	REACT_6900:Signaling in Immune system	39	4.67E-14	3.81	2.10E-12
GOTERM_CC_FAT	GO:0005576~extracellular region	121	1.17E-13	1.95	4.36E-11
GOTERM_CC_FAT	GO:0016021~integral to membrane	284	1.53E-11	1.37	1.91E-09
GOTERM_BP_FAT	GO:0006954~inflammatory response	37	5.59E-10	3.18	4.83E-07
KEGG_PATHWAY	hsa04940:Type I diabetes mellitus	12	2.88E-08	7.89	4.49E-06
GOTERM_BP_FAT	GO:0022610~biological adhesion	65	1.29E-08	2.09	4.76E-06
KEGG_PATHWAY	hsa05320:Autoimmune thyroid disease	10	6.15E-08	9.61	4.80E-06
KEGG_PATHWAY	hsa05332:Graft-versus-host disease	10	1.60E-07	8.92	5.00E-06
KEGG_PATHWAY	hsa05330:Allograft rejection	10	1.60E-07	8.92	5.00E-06
GOTERM_BP_FAT	GO:0007155~cell adhesion	65	1.16E-08	2.10	5.03E-06
KEGG_PATHWAY	hsa05310:Asthma	8	1.42E-07	12.49	5.53E-06
KEGG_PATHWAY	hsa05416:Viral myocarditis	15	2.84E-06	4.36	5.53E-05
KEGG_PATHWAY	hsa05322:Systemic lupus erythematosus	14	3.47E-06	4.60	6.01E-05
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	35	2.79E-07	2.63	2.30E-04
REACTOME_PATHWAY	REACT_604:Hemostasis	27	1.06E-05	2.50	2.38E-04
KEGG_PATHWAY	hsa04610:Complement and coagulation cascades	12	2.67E-05	4.54	4.16E-04
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	13	2.91E-06	5.16	5.03E-04
GOTERM_BP_FAT	GO:0006909~phagocytosis	12	1.42E-05	4.91	2.05E-03
GOTERM_BP_FAT	GO:0002526~acute inflammatory response	14	3.00E-05	3.94	4.09E-03
KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	11	3.45E-04	3.82	4.48E-03
KEGG_PATHWAY	hsa04360:Axon guidance	20	3.30E-04	2.45	4.66E-03
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	84	5.23E-05	1.54	5.64E-03
GOTERM_BP_FAT	GO:0042110~T cell activation	17	7.78E-05	3.10	7.73E-03

By contrast, the genes that are more highly expressed in the arachnoidal cells than in the meningiomas reveal enrichment in pathways related to extracellular matrix, cytoskeleton and adhesion (Table 5) which could reflect the either upregulation of such genes under *in vitro* culture conditions or the presence of merlin in the arachnoidal cells, or both.

Table 5- Top pathways enriched for genes more highly expressed in the merlin-expressing arachnoidal cell line than in merlin-deficient meningiomas

Category	Term	Count	PValue	Fold Enrichment	Benjamini P-Value
GOTERM_CC_FAT	GO:0005576~extracellular region	47	5.30E-08	2.31	1.53E-05
GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	19	1.39E-06	3.91	2.01E-04
GOTERM_CC_FAT	GO:0005604~basement membrane	10	1.45E-05	6.70	6.96E-04
GOTERM_CC_FAT	GO:0044420~extracellular matrix part	12	9.83E-06	5.48	7.10E-04
GOTERM_CC_FAT	GO:0070161~anchoring junction	14	1.30E-05	4.46	7.51E-04
GOTERM_CC_FAT	GO:0005912~adherens junction	13	2.74E-05	4.50	1.13E-03
GOTERM_CC_FAT	GO:0005886~plasma membrane	71	4.90E-05	1.55	1.77E-03
GOTERM_CC_FAT	GO:0031012~extracellular matrix	17	6.08E-05	3.25	1.95E-03
GOTERM_CC_FAT	GO:0000267~cell fraction	35	9.65E-05	2.01	2.32E-03
GOTERM_CC_FAT	GO:0044459~plasma membrane part	51	9.05E-05	1.71	2.38E-03
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	16	8.28E-05	3.33	2.39E-03
GOTERM_CC_FAT	GO:0005856~cytoskeleton	42	1.98E-04	1.79	4.39E-03
GOTERM_CC_FAT	GO:0044449~contractile fiber part	9	3.11E-04	5.17	6.40E-03
GOTERM_CC_FAT	GO:0043292~contractile fiber	9	4.15E-04	4.95	7.97E-03
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	12	5.32E-04	3.54	9.56E-03

A major difficulty in more detailed analysis was the lack of a normal *in vivo* arachnoidal tissue comparator due to the failure of all autopsy specimens. This fact, combined with the lack of individual meningioma progression genes emerging from the exome analyses of Task 1 prompted us to focus our efforts on expanding the RNAseq runs with additional replicates of the cultured arachnoidal cells in order to achieve more reliable, robust statistics and to better define the consequences of merlin loss in these isogenic cells, without the confound of other germline or somatic genetic variation. We added triplicate analyses of paired merlin heterozygous and merlin null arachnoidal cells and performed deep RNAseq analysis. To identify statistically differentially expressed (DE) genes from the pairwise comparison we applied the bioconductor package edgeR (v. 3.12.0) on the R platform (v. 3.2.2) to raw count data as expression values using a quasi-likelihood F-test. Significant DE genes were identified at varying stringency levels including nominal p-value < 0.05, Benjamini-Hochberg FDR < 0.05 and Bonferroni FDR < 0.05 (Figure 3).



Genes analyzed	15417		
Categories	**All**	**Up**	**Down**
p < 0.05	3523	1616	1907
Adj. p (BH) < 0.05	1969	844	1125
Adj. p (bonf) < 0.05	501	181	320

Figure 3 – Differential expression of genes in merlin-null compared with merlin-heterozygous arachnoidal cells at different levels of statistical significance

Under the most stringent conditions, this analysis revealed 181 genes and 320 genes significantly up-regulated or down-regulated, respectively, by merlin deficiency (these differentially expressed genes are given in the Appendix). Among the up-regulated genes were kinases and other genes that could constitute novel targets for therapeutic intervention in meningiomas. These include genes encoding members of the ephrin family of receptors, *EPH4* and *EPHB1*, which were consistently upregulated 3 ($p=7.9 \times 10^{-9}$) and 2.7 fold ($p=1.2 \times 10^{-3}$). A publication summarizing these data is being prepared in conjunction with pathway analyses of the data (see Aim 3) and preliminary testing of potential drug targets so identified in collaboration with the Children's Tumor Foundation NF2 Synodos Consortium.

Task 3. Identification and validation of genes contributing to tumorigenesis

This task was directed at identifying the genes/pathways implicated by somatic alterations as cooperating in meningioma tumor formation or progression to a higher grade tumor and then manipulating those genes using lentiviral-delivered short-hairpin RNAs (shRNA) to specifically suppress the expression of target genes. After funding of the grant, CRISPR/Cas9 genome editing became available to reliably inactivate one or both copies of the locus in question, enabling us to mutate the *NF2* gene and providing us with a technique to obviate shRNA suppression for progression genes. Unfortunately, our data in Aim 1 pointed to the involvement of broad chromosomal regions in progression of meningiomas and did not support the critical importance of any specific genes within these regions. Rather, the development of meningiomas is marked with chromosome instability that favors some genomic regions, but whether this is a direct result of merlin deficiency, or a simple consequence of ascertainment of these events due to their contribution to meningioma cell growth is not clear. While it may theoretically be possible to recreate these chromosomal events in arachnoidal cell lines using CRISPR/Cas9 manipulation, this strategy is not nearly as straightforward as inactivating individual genes and is outside the scope of this grant. However, our work does suggest that the manipulation of chromosome structure using CRISPR/Cas9 may be a useful direction in the future investigation of meningioma mechanisms [25].

While our project did not reveal specific progression genes mutated in meningioma, the gene expression analyses did point to particular genes that are differentially expressed as a result of merlin loss as potential targets for therapeutic intervention as noted under Aim 2. To determine whether the differentially expressed genes from our more robust analysis of the cultured arachnoidal lines clustered into particular functional pathways, we also performed pathway analysis using DAVID (v. 6.7). All analyzed genes were used as a background gene list to define Gene Ontology and pathway terms enriched at Bonferroni FDR < 0.05 for significant DE genes, assembled distinctly for up-regulated, down-regulated and combined DE genes. The results of these analyses are given in Table 6. Notably, the mitochondria-related pathways from the original small-scale analysis disappeared from the list enriched for upregulated genes, to be replaced by far more statistically significant pathways related to extracellular regions and to mitosis (e.g., top pathway P =1.83E-11 versus 3.52E-03 in the previous analysis). Notably, the cation/metal binding pathways disappeared from the list of pathways enriched for downregulated genes, which is now topped at 2.4E-24 by the same term, GO:0005576~extracellular region, that shows the top enrichment for upregulated genes. Thus, the pathways represented by GO:0005576~extracellular region are highly dysregulated, with some elements increasing and some decreasing in expression due to merlin loss. When both up- and down-regulated genes are considered together in the pathway analysis, GO:0005576~extracellular region achieves a Benjamini-Hochberg corrected P value of 2.89E-40 confirming the strong enrichment for dysregulated genes, regardless of direction (Table 7). In considering all dysregulated genes, terms related to mitosis fall from their position near the top of pathways enriched for upregulated genes, being replaced near the top of the list by terms related to the extracellular space and matrix, cell adhesion, plasma membrane and integral/intrinsic membrane proteins. This analysis suggests that loss of merlin has major consequences for the interaction between arachnoidal cells and their environment/neighbors and that this disruption is likely to be intimately tied to tumor development due to *NF2* inactivation. It also points to the future potential for using cellular assays based upon extracellular matrix/cell adhesion and activation of particular signaling pathways for drug screening in NF2 and sporadic meningioma, targeting the differential between merlin-expressing and merlin-null arachnoidal cells. A publication reporting these pathway data is being prepared in conjunction with the individual gene DE analysis data (see Aim 2) along with preliminary testing of potential drug targets identified in collaboration with the Children's Tumor Foundation NF2 Synodos Consortium.

Table 6- Top pathways enriched for genes upregulated and downregulated due to merlin loss in expanded arachnoidal cell RNA sequencing data

Effect	Category	Term	Count	PValue	Fold Enrichment	Benjamini P value
Upregulated	GOTERM_BP_FAT	GO:0005576~extracellular region	73	5.76E-14	2.53	1.83E-11
Upregulated	GOTERM_BP_FAT	GO:0044421~extracellular region part	51	1.93E-13	3.19	3.08E-11
Upregulated	GOTERM_BP_FAT	GO:0000279~M phase	36	2.13E-09	3.15	1.23E-06
Upregulated	GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	31	1.14E-09	3.65	1.32E-06
Upregulated	GOTERM_BP_FAT	GO:0048285~organelle fission	31	1.80E-09	3.58	1.39E-06
Upregulated	GOTERM_BP_FAT	GO:0007067~mitosis	31	7.08E-10	3.72	1.64E-06
Upregulated	GOTERM_BP_FAT	GO:0000280~nuclear division	31	7.08E-10	3.72	1.64E-06
Upregulated	GOTERM_BP_FAT	GO:0005615~extracellular space	31	3.31E-08	3.15	2.64E-06
Upregulated	GOTERM_BP_FAT	GO:0031012~extracellular matrix	27	2.77E-08	3.55	2.94E-06
Upregulated	GOTERM_BP_FAT	GO:0051301~cell division	33	1.63E-08	3.11	7.53E-06
Upregulated	GOTERM_BP_FAT	GO:0005819~spindle	22	2.05E-07	3.82	1.31E-05
Upregulated	GOTERM_BP_FAT	GO:0005578~proteinaceous extracellular matrix	24	3.52E-07	3.44	1.87E-05
Upregulated	GOTERM_BP_FAT	GO:0005886~plasma membrane	107	6.21E-07	1.54	2.83E-05
Upregulated	GOTERM_BP_FAT	GO:0022403~cell cycle phase	38	1.13E-07	2.61	4.35E-05
Upregulated	GOTERM_BP_FAT	GO:0022610~biological adhesion	37	5.37E-07	2.50	1.13E-04
Upregulated	GOTERM_BP_FAT	GO:0051048~negative regulation of secretion	9	5.33E-07	11.12	1.23E-04
Upregulated	GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	36	4.27E-07	2.56	1.24E-04
Upregulated	GOTERM_BP_FAT	GO:0022402~cell cycle process	45	3.88E-07	2.26	1.28E-04
Upregulated	GOTERM_BP_FAT	GO:0007155~cell adhesion	37	5.03E-07	2.50	1.29E-04
Upregulated	GOTERM_BP_FAT	GO:0051783~regulation of nuclear division	12	9.10E-07	6.74	1.76E-04
Upregulated	GOTERM_BP_FAT	GO:0007088~regulation of mitosis	12	9.10E-07	6.74	1.76E-04
Upregulated	GOTERM_BP_FAT	GO:0008083~growth factor activity	14	5.75E-07	5.76	2.91E-04
Upregulated	GOTERM_BP_FAT	GO:0044459~plasma membrane part	74	9.97E-06	1.64	3.97E-04
Upregulated	GOTERM_BP_FAT	GO:0009986~cell surface	21	1.51E-05	3.05	5.34E-04
Upregulated	GOTERM_BP_FAT	GO:0001525~angiogenesis	17	3.62E-06	4.04	6.44E-04
Downregulatec	GOTERM_CC_FAT	GO:0005576~extracellular region	135	6.46E-27	2.57	2.40E-24
Downregulatec	GOTERM_CC_FAT	GO:0044421~extracellular region part	88	5.74E-22	3.02	1.07E-19
Downregulatec	GOTERM_CC_FAT	GO:0005886~plasma membrane	214	2.04E-18	1.70	2.52E-16
Downregulatec	GOTERM_CC_FAT	GO:0031012~extracellular matrix	51	1.65E-16	3.68	1.03E-14
Downregulatec	GOTERM_BP_FAT	GO:0022610~biological adhesion	75	1.90E-17	2.90	2.41E-14
Downregulatec	GOTERM_BP_FAT	GO:0007155~cell adhesion	75	1.62E-17	2.91	4.11E-14
Downregulatec	GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	48	5.98E-16	3.78	4.12E-14
Downregulatec	GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	104	9.70E-16	2.25	8.44E-13
Downregulatec	GOTERM_CC_FAT	GO:0016021~integral to membrane	271	7.51E-14	1.44	4.64E-12
Downregulatec	GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	277	1.44E-13	1.42	7.62E-12
Downregulatec	GOTERM_MF_FAT	GO:0005509~calcium ion binding	80	1.23E-14	2.50	9.43E-12
Downregulatec	GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	81	3.69E-12	2.23	1.71E-10
Downregulatec	GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	82	4.68E-12	2.21	1.93E-10
Downregulatec	GOTERM_CC_FAT	GO:0005615~extracellular space	48	4.25E-10	2.68	1.58E-08
Downregulatec	GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	43	8.39E-11	3.04	5.32E-08
Downregulatec	GOTERM_CC_FAT	GO:0044459~plasma membrane part	132	6.30E-09	1.61	2.13E-07
Downregulatec	GOTERM_BP_FAT	GO:0016339~calcium-dependent cell-cell adhesion	12	6.22E-10	10.61	3.15E-07
Downregulatec	GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	31	7.80E-09	3.30	2.82E-06
Downregulatec	GOTERM_BP_FAT	GO:0007156~homophilic cell adhesion	21	7.04E-09	4.64	2.97E-06
Downregulatec	GOTERM_BP_FAT	GO:0001501~skeletal system development	36	3.61E-08	2.80	1.14E-05
Downregulatec	GOTERM_BP_FAT	GO:0043062~extracellular structure organization	27	6.20E-08	3.35	1.74E-05
Downregulatec	GOTERM_BP_FAT	GO:0050877~neurological system process	52	7.60E-08	2.22	1.93E-05
Downregulatec	PANTHER_PATHWAY	P00012:Cadherin signaling pathway	23	6.19E-07	3.18	5.38E-05
Downregulatec	GOTERM_BP_FAT	GO:0007416~synaptogenesis	11	2.75E-07	7.78	5.80E-05
Downregulatec	GOTERM_BP_FAT	GO:0007267~cell-cell signaling	39	2.62E-07	2.47	6.04E-05
Downregulatec	REACTOME_PATHWA	REACT_14797:Signaling by GPCR	16	5.41E-06	3.93	1.89E-04
Downregulatec	GOTERM_MF_FAT	GO:0030246~carbohydrate binding	30	7.42E-07	2.77	2.84E-04
Downregulatec	GOTERM_CC_FAT	GO:0044420~extracellular matrix part	19	9.22E-06	3.31	2.85E-04
Downregulatec	GOTERM_CC_FAT	GO:0005581~collagen	11	2.31E-05	5.14	6.59E-04

Table 7- Top pathways enriched for genes dysregulated (regardless of direction) due to merlin loss in expanded arachnoidal cell RNA sequencing data

Category	Term	Count	PValue	Fold Enrichment	Benjamini P value
GOTERM_CC_FAT	GO:0005576~extracellular region	208	6.41E-43	2.56	2.89E-40
GOTERM_CC_FAT	GO:0044421~extracellular region part	139	1.42E-37	3.08	3.20E-35
GOTERM_CC_FAT	GO:0031012~extracellular matrix	78	2.78E-26	3.64	4.18E-24
GOTERM_CC_FAT	GO:0005886~plasma membrane	321	4.22E-25	1.64	4.76E-23
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	72	1.80E-24	3.66	1.63E-22
GOTERM_BP_FAT	GO:0022610~biological adhesion	112	6.63E-25	2.75	1.10E-21
GOTERM_BP_FAT	GO:0007155~cell adhesion	112	5.15E-25	2.76	1.70E-21
GOTERM_CC_FAT	GO:0005615~extracellular space	79	7.50E-19	2.85	5.63E-17
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	149	4.77E-19	2.05	5.25E-16
GOTERM_MF_FAT	GO:0005509~calcium ion binding	113	3.63E-18	2.29	3.41E-15
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	121	2.63E-16	2.10	1.43E-14
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	118	6.83E-16	2.10	3.75E-14
GOTERM_CC_FAT	GO:0044459~plasma membrane part	206	3.85E-14	1.62	1.93E-12
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	403	5.19E-14	1.33	2.34E-12
GOTERM_CC_FAT	GO:0016021~integral to membrane	391	1.06E-13	1.34	4.35E-12
GOTERM_BP_FAT	GO:0043062~extracellular structure organization	41	8.36E-12	3.24	6.91E-09
GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signaling pathway	57	2.19E-11	2.56	1.45E-08
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	47	5.09E-11	2.82	2.39E-08
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	43	1.22E-10	2.91	6.72E-08
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	58	7.06E-10	2.34	3.33E-07
GOTERM_MF_FAT	GO:0001871~pattern binding	29	1.72E-09	3.52	5.38E-07
GOTERM_MF_FAT	GO:0030247~polysaccharide binding	29	1.72E-09	3.52	5.38E-07
GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	27	3.62E-09	3.62	8.52E-07

Key Research Accomplishments

Completion and analysis of exome sequencing of 126 samples representing human tumor (meningioma or schwannoma) and normal DNAs from the same individuals, identifying chromosome rearrangement with broad dosage change as the primary somatic genetic event in meningioma after NF2 inactivation, in contrast to schwannoma where exonic point mutation may play a greater role in tumor growth/progression.

Generation and analysis of RNAseq data from the meningiomas used for exome sequencing identifying probably immune cell infiltration within these tumors and confirming SGK1 as a potential therapeutic target.

Generation and analysis of RNAseq data from isogenic arachnoidal cells with or without inactivation of *NF2*, generated using CRISPR/Cas genome editing technology, defining genes and pathways showing specific altered expression due to merlin loss and implicating EPH4 and EPHB1 as potential therapeutic targets.

Conclusion

Exome analysis of meningiomas and schwannomas suggest a different genetic architecture beyond the common element of merlin inactivation in the genesis of these NF2-associated tumor types. Meningiomas display considerable chromosomal rearrangement leading to dosage change of large chromosome regions without implicating specific genes within these regions. By contrast, schwannomas show more frequent evidence of potential cooperating genes altered by point mutation. The gene expression analysis of meningiomas is complicated by the lack of a true control tissue and the evidence for immune cell infiltration, but does confirm serum/glucocorticoid-regulated kinase 1, identified previously in a kinase RNAi suppression screen as a potential target for therapeutic intervention. Use of CRISPR/Cas-edited arachnoidal cells to compare complete merlin inactivation with the heterozygous inactivation seen in NF2 provided isogenic lines that avoided the genetic heterogeneity in human tumors and revealed a number of new potential therapeutic targets, including ephrin family receptor kinases encoded by *EPH4* and *EPHB1*. Loss of merlin coincided with upregulation of a variety of pathways involved with extracellular matrix, cell adhesion and membrane proteins along with sets of genes regulated by MYC and MTORC1. These molecular data provide a foundation for

targeting particular kinases for potential therapeutic intervention in NF2/meningioma and inform the future development of potential drug screening assays to reverse the effects of merlin loss.

Publications, abstracts and presentations

Two publications are in preparation reporting the findings of Aim 1 and Aims2+3, respectively.

Inventions, patents and Licenses

None

Reportable Outcomes

The planned publications will report 1) the knowledge that no frequent single gene mutational events are frequent in meningioma development which, after merlin loss, is associated with considerable chromosomal instability leading to dosage alterations of broad chromosomal regions; 2) the finding that *EPH4* and *EPHB1* may prove to be effective drug targets for NF2/meningioma and 3) the potential for functional assays directly relevant to the molecular and cellular effects of merlin loss as the basis for screens to reverse these deficits and thereby open new therapeutic avenues.

Other Achievements

This project enabled us to join in a large collaboration, the Children's Tumor Foundation-sponsored NF2 Synodos Consortium, aimed at cooperative testing of potential NF2 therapeutics in cell culture and in mouse models, in anticipation of development a human clinical trial.

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Appendices

List of genes upregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

List of genes downregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

List of genes robustly upregulated by *NF2* inactivation in cultured arachnoidal cells in our expanded data set

List of genes robustly downregulated by *NF2* inactivation in cultured arachnoidal cells in our expanded data set

List of genes upregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

Gene Symbol	ENSEMBL ID	mean fold change	sd	Z score
DPP3	ENSG00000254986	0.39	0.0007	579.83
SGK1	ENSG00000118515	1.29	0.0026	491.48
ATAD3C	ENSG00000215915	0.47	0.0018	253.55
CCT5	ENSG00000150753	0.69	0.0042	165.42
WDR43	ENSG00000163811	0.44	0.0030	145.22
NLK	ENSG00000087095	0.96	0.0069	139.26
KLC1	ENSG00000256500	0.49	0.0048	102.47
GPATCH4	ENSG00000160818	0.63	0.0068	92.28
TAGLN2P1	ENSG00000253676	0.87	0.0102	85.87
SLC35B4	ENSG00000205060	0.60	0.0075	79.74
CCDC167	ENSG00000198937	0.60	0.0078	76.52
NOP56	ENSG00000101361	0.54	0.0075	72.24
NME1	ENSG00000239672	0.81	0.0112	72.22
TPI1P1	ENSG00000226415	0.48	0.0069	70.47
MRPL22	ENSG00000082515	0.50	0.0074	67.65
SEC23B	ENSG00000101310	0.68	0.0103	66.29
MPV17L2	ENSG00000254858	0.52	0.0080	64.43
ARMCX2	ENSG00000184867	3.96	0.0625	63.34
CORO1C	ENSG00000110880	0.56	0.0089	63.04
FDXR	ENSG00000161513	0.90	0.0143	62.83
TNFSF9	ENSG00000125657	3.72	0.0597	62.25
ME2	ENSG00000082212	0.73	0.0121	60.17
PTPN1	ENSG00000196396	0.52	0.0088	59.39
BRIX1	ENSG00000113460	0.55	0.0097	56.75
DNAJC22	ENSG00000178401	0.65	0.0122	53.12
SENP3-EIF4A1	ENSG00000265500	0.45	0.0087	52.52
ARL6IP1	ENSG00000170540	0.56	0.0107	52.40
CCT3	ENSG00000163468	0.46	0.0087	52.23
NDUFAB1	ENSG00000004779	0.51	0.0100	51.16
TPI1	ENSG00000111669	0.52	0.0102	50.89
EPHA2	ENSG00000142627	0.74	0.0146	50.26
AP1B1	ENSG00000100280	0.55	0.0111	50.11
FAM216A	ENSG00000204856	1.08	0.0219	49.63
FAM122B	ENSG00000156504	0.49	0.0102	48.26
GOT2	ENSG00000125166	0.48	0.0101	47.77
PRMT5	ENSG00000100462	0.68	0.0143	47.46
FAM86B3P	ENSG00000173295	1.37	0.0293	46.94
RBMS2P1	ENSG00000213250	0.54	0.0118	45.85
RP2	ENSG00000102218	0.63	0.0142	44.51
KIF4B	ENSG00000226650	1.52	0.0344	44.24
PSMD2	ENSG00000175166	0.48	0.0113	42.26
UBE2M	ENSG00000130725	0.50	0.0118	42.21
UHMK1	ENSG00000152332	0.56	0.0134	41.44

List of genes upregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

CHAMP1	ENSG00000198824	0.60	0.0146	41.32
OGFOD1	ENSG00000087263	0.44	0.0106	41.04
UCK2	ENSG00000143179	0.88	0.0217	40.58
GEMIN7	ENSG00000142252	0.55	0.0136	40.16
STARD8	ENSG00000130052	0.99	0.0248	40.14
PPP1R35	ENSG00000160813	0.39	0.0100	38.66
RP11-552M11.4	ENSG00000243960	0.74	0.0190	38.65
PRKX	ENSG00000183943	0.85	0.0221	38.55
ZNF668	ENSG00000167394	0.57	0.0151	37.97
MATN2	ENSG00000132561	1.68	0.0443	37.89
GAPDH	ENSG00000111640	0.47	0.0124	37.74
CTD-2066L21.2	ENSG00000251281	1.65	0.0441	37.37
ACTN1	ENSG00000072110	0.67	0.0181	37.09
ATP13A2	ENSG00000159363	0.65	0.0176	36.94
ABHD12	ENSG00000100997	0.98	0.0266	36.89
CDKN1A	ENSG00000124762	0.81	0.0222	36.52
BAX	ENSG00000087088	0.60	0.0168	35.65
MARCH4	ENSG00000144583	3.02	0.0848	35.57
NIN	ENSG00000100503	0.41	0.0117	35.41
TCEB1	ENSG00000154582	0.39	0.0111	35.20
MRPL24	ENSG00000143314	0.41	0.0116	35.12
SDPR	ENSG00000168497	1.28	0.0363	35.12
PARVA	ENSG00000197702	0.53	0.0150	35.10
KIF20A	ENSG00000112984	1.07	0.0308	34.82
MYEOV	ENSG00000172927	3.03	0.0872	34.80
TIMM10	ENSG00000134809	0.58	0.0168	34.78
SPA17	ENSG00000064199	1.35	0.0392	34.40
GEMIN6	ENSG00000152147	0.59	0.0172	34.22
XPO6	ENSG00000169180	0.42	0.0123	33.71
KLC1	ENSG00000126214	0.47	0.0141	33.25
ARL17A	ENSG00000185829	0.61	0.0184	33.01
RP4-614O4.11	ENSG00000261582	0.45	0.0137	32.99
WDR4	ENSG00000160193	0.71	0.0214	32.94
CLPTM1L	ENSG00000049656	0.55	0.0168	32.70
NFU1	ENSG00000169599	0.41	0.0126	32.48
CKS2	ENSG00000123975	0.81	0.0254	31.99
APEX2	ENSG00000169188	0.67	0.0212	31.77
NALCN	ENSG00000102452	1.10	0.0345	31.72
U47924.19	ENSG00000255896	0.66	0.0210	31.45
ALKBH6	ENSG00000239382	0.39	0.0125	31.33
ZFP3	ENSG00000180787	0.60	0.0193	31.29
CRIM1	ENSG00000150938	0.74	0.0237	31.28
CLDN1	ENSG00000163347	2.92	0.0934	31.22
PTCD1	ENSG00000106246	0.42	0.0134	31.15
SFTA1P	ENSG00000225383	4.68	0.1509	31.00
NCAPD2	ENSG00000010292	0.74	0.0239	30.99

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SCO1	ENSG00000133028	0.51	0.0166	30.61
LMO3	ENSG00000048540	1.82	0.0595	30.59
DNAJC11	ENSG00000007923	0.77	0.0255	30.32
CHCHD3	ENSG00000106554	0.38	0.0126	30.18
APEH	ENSG00000164062	0.53	0.0177	30.09
SNRPF	ENSG00000139343	0.44	0.0149	29.69
RP11-186B7.4	ENSG00000264772	0.43	0.0144	29.63
CITED2	ENSG00000164442	0.97	0.0330	29.25
HOMER3	ENSG00000051128	0.65	0.0223	28.97
CCT7	ENSG00000135624	0.49	0.0169	28.93
CD3EAP	ENSG00000117877	0.97	0.0336	28.77
TFE3	ENSG00000068323	0.45	0.0156	28.75
AXL	ENSG00000167601	1.14	0.0399	28.69
ARHGAP22	ENSG00000128805	1.66	0.0582	28.52
PPM1G	ENSG00000115241	0.41	0.0144	28.46
AKAP2	ENSG00000241978	0.45	0.0158	28.45
SF3B3	ENSG00000189091	0.39	0.0138	28.39
PSMG1	ENSG00000183527	0.62	0.0220	28.28
KRTAP1-5	ENSG00000221852	2.75	0.0978	28.09
COA4	ENSG00000181924	0.41	0.0149	27.77
KIRREL3	ENSG00000149571	1.72	0.0624	27.52
PPP6C	ENSG00000119414	0.43	0.0158	27.48
FAM46B	ENSG00000158246	2.32	0.0850	27.25
CCDC107	ENSG00000159884	0.47	0.0172	27.12
PIM3	ENSG00000198355	0.50	0.0186	27.07
GGH	ENSG00000137563	0.78	0.0290	27.04
BUB3	ENSG00000154473	0.67	0.0249	27.03
TDRKH	ENSG00000182134	0.89	0.0330	26.98
SERPINB7	ENSG00000166396	2.29	0.0850	26.92
DUSP14	ENSG00000161326	0.86	0.0319	26.84
CDKN3	ENSG00000100526	1.25	0.0467	26.71
MON1A	ENSG00000164077	0.39	0.0144	26.70
EIF2S2P3	ENSG00000236493	1.04	0.0391	26.66
FARSB	ENSG00000116120	0.61	0.0232	26.43
HIGD1A	ENSG00000181061	0.43	0.0163	26.41
RNF167	ENSG00000108523	0.42	0.0160	26.21
C6orf211	ENSG00000146476	0.63	0.0240	26.18
ZFP91-CNTF	ENSG00000255073	0.53	0.0204	25.97
MLX	ENSG00000108788	0.58	0.0226	25.86
CTNNAL1	ENSG00000119326	1.33	0.0521	25.54
GCAT	ENSG00000100116	0.66	0.0259	25.48
ADPRHL2	ENSG00000116863	0.49	0.0192	25.46
SNRPC	ENSG00000124562	0.45	0.0179	25.34
ATIC	ENSG00000138363	0.61	0.0240	25.25
SRF	ENSG00000112658	0.40	0.0157	25.24
CTD-2066L21.3	ENSG00000250697	1.67	0.0661	25.20

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WBP4	ENSG00000120688	0.42	0.0166	25.08
PAM16	ENSG00000217930	0.47	0.0189	24.77
CCT2	ENSG00000166226	0.44	0.0178	24.71
IMP3	ENSG00000177971	0.83	0.0337	24.70
SH3RF1	ENSG00000154447	1.26	0.0509	24.68
DDB2	ENSG00000134574	0.88	0.0356	24.68
FGF1	ENSG00000113578	2.67	0.1084	24.62
PKM	ENSG00000067225	0.68	0.0277	24.37
CFL1	ENSG00000172757	0.58	0.0238	24.23
EPB41L2	ENSG00000079819	0.78	0.0322	24.18
ASCC2	ENSG00000100325	0.40	0.0167	24.15
DARS2	ENSG00000117593	0.61	0.0253	24.14
IER3IP1	ENSG00000267228	0.39	0.0163	24.12
NUDCD1	ENSG00000120526	0.84	0.0349	24.11
GOLGA4	ENSG00000144674	0.44	0.0184	23.91
C17orf89	ENSG00000224877	0.54	0.0227	23.77
RCC1	ENSG00000180198	0.56	0.0235	23.63
CRY1	ENSG00000008405	0.82	0.0349	23.56
AC004797.1	ENSG00000229944	0.52	0.0222	23.50
DDAH1	ENSG00000153904	0.86	0.0369	23.45
OGDH	ENSG00000105953	0.45	0.0191	23.38
RP11-21J18.1	ENSG00000265257	0.40	0.0169	23.36
NDUFV2	ENSG00000178127	0.41	0.0175	23.25
TEAD4	ENSG00000197905	0.67	0.0289	23.21
ALS2CL	ENSG00000178038	1.69	0.0731	23.14
MRPS12	ENSG00000128626	0.67	0.0290	23.14
SH2B3	ENSG00000111252	0.39	0.0169	23.09
CLIC3	ENSG00000169583	0.66	0.0287	23.05
ENO1	ENSG00000074800	0.76	0.0334	22.79
RND3	ENSG00000115963	1.41	0.0623	22.62
CNOT7	ENSG00000198791	0.40	0.0178	22.41
KRT34	ENSG00000131737	3.47	0.1563	22.18
DHRS2	ENSG00000100867	1.99	0.0899	22.17
PPAT	ENSG00000128059	0.53	0.0240	22.12
NIPAL3	ENSG00000001461	1.91	0.0872	21.93
CCBE1	ENSG00000183287	2.76	0.1261	21.91
FERMT2	ENSG00000073712	0.46	0.0212	21.86
RUVBL2	ENSG00000183207	0.80	0.0366	21.85
METAP1	ENSG00000164024	0.52	0.0237	21.82
ARHGAP23	ENSG00000225485	0.58	0.0269	21.58
POLDIP2	ENSG00000004142	0.52	0.0246	21.26
TPGS2	ENSG00000134779	0.60	0.0282	21.11
STPG1	ENSG00000001460	1.07	0.0513	20.91
C6orf132	ENSG00000188112	1.19	0.0568	20.91
MRPL46	ENSG00000259494	0.44	0.0213	20.84
APRT	ENSG00000198931	0.51	0.0243	20.79

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EDN1	ENSG00000078401	2.14	0.1028	20.77
KRT7	ENSG00000135480	0.99	0.0480	20.67
PCID2	ENSG00000126226	0.59	0.0288	20.66
EVA1A	ENSG00000115363	1.14	0.0554	20.62
NUP88	ENSG00000108559	0.61	0.0297	20.58
ARMC1	ENSG00000104442	0.41	0.0199	20.53
LRRC8D	ENSG00000171492	1.05	0.0515	20.45
POLR3K	ENSG00000161980	0.83	0.0408	20.41
DNAJC8	ENSG00000126698	0.59	0.0290	20.35
HERC4	ENSG00000148634	1.24	0.0615	20.17
FARSA	ENSG00000179115	0.52	0.0258	20.15
MYBL1	ENSG00000185697	1.30	0.0650	20.07
MPP4	ENSG00000082126	1.33	0.0667	20.03
NEIL3	ENSG00000109674	1.07	0.0534	20.00
PIF1	ENSG00000140451	1.23	0.0613	19.99
HEXB	ENSG00000049860	0.41	0.0204	19.96
ZFP91	ENSG00000186660	0.48	0.0242	19.90
SIPA1L3	ENSG00000105738	0.38	0.0192	19.75
USMG5	ENSG00000173915	0.39	0.0199	19.69
GEMIN2	ENSG00000092208	0.40	0.0202	19.67
EIF4A1	ENSG00000161960	0.39	0.0198	19.63
MRPL44	ENSG00000135900	0.56	0.0289	19.44
SLC25A1	ENSG00000100075	0.50	0.0259	19.43
HSPBP1	ENSG00000133265	0.38	0.0197	19.36
PGAM1	ENSG00000171314	0.81	0.0420	19.29
FLNC	ENSG00000128591	0.74	0.0388	19.14
MRPL35	ENSG00000132313	0.48	0.0251	19.13
MRPS23	ENSG00000181610	0.47	0.0249	19.06
KNSTRN	ENSG00000128944	1.35	0.0708	19.03
CTD-2037K23.2	ENSG00000245556	0.61	0.0323	19.02
KIAA1432	ENSG00000107036	0.52	0.0274	19.01
EIF2B3	ENSG00000070785	0.64	0.0339	19.00
ERCC2	ENSG00000104884	1.19	0.0629	18.95
NHP2	ENSG00000145912	0.57	0.0302	18.94
SOX6	ENSG00000110693	6.22	0.3291	18.91
MRPS18C	ENSG00000163319	0.41	0.0218	18.88
SRSF1	ENSG00000136450	0.48	0.0253	18.78
CAV1	ENSG00000105974	1.37	0.0727	18.78
RTCA	ENSG00000137996	0.41	0.0219	18.77
SORBS3	ENSG00000120896	0.63	0.0337	18.73
PTTG1	ENSG00000164611	1.17	0.0625	18.70
COPS6	ENSG00000168090	0.56	0.0299	18.61
SNHG10	ENSG00000247092	0.61	0.0330	18.55
KIAA1107	ENSG00000069712	0.80	0.0434	18.46
GBE1	ENSG00000114480	0.39	0.0211	18.41
MET	ENSG00000105976	1.39	0.0758	18.34

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STX2	ENSG00000111450	0.52	0.0285	18.31
AOX1	ENSG00000138356	1.99	0.1091	18.27
OAZ1	ENSG00000104904	0.54	0.0297	18.20
GDF11	ENSG00000135414	0.49	0.0272	18.17
ESD	ENSG00000139684	0.63	0.0347	18.10
VTA1	ENSG00000009844	0.48	0.0265	18.09
PSMG4	ENSG00000180822	0.55	0.0306	18.07
STK32B	ENSG00000152953	1.11	0.0614	18.03
C8orf58	ENSG00000241852	0.55	0.0308	17.88
TNFAIP1	ENSG00000109079	1.04	0.0580	17.86
MAP7D3	ENSG00000129680	0.56	0.0311	17.84
ANXA2P2	ENSG00000231991	0.65	0.0367	17.77
EZR	ENSG00000092820	1.28	0.0720	17.77
RWDD2B	ENSG00000156253	0.47	0.0267	17.67
KM-PA-2	ENSG00000204775	0.63	0.0358	17.62
RP11-392A22.2	ENSG00000240875	0.71	0.0400	17.62
CCNB1	ENSG00000134057	1.25	0.0707	17.62
NEK7	ENSG00000151414	1.66	0.0943	17.59
CARD10	ENSG00000100065	0.93	0.0530	17.58
IRS1	ENSG00000169047	1.52	0.0868	17.53
ZDHHC16	ENSG00000171307	0.48	0.0276	17.51
DNAJC6	ENSG00000116675	2.70	0.1544	17.46
GYG1	ENSG00000163754	1.10	0.0634	17.39
METTL3	ENSG00000165819	0.38	0.0220	17.37
RP11-488C13.1	ENSG00000241081	0.52	0.0303	17.31
ISOC2	ENSG00000063241	0.54	0.0315	17.25
SLC25A17	ENSG00000100372	0.38	0.0220	17.23
TSFM	ENSG00000123297	0.42	0.0241	17.21
RNF144B	ENSG00000137393	1.03	0.0597	17.19
TTC9C	ENSG00000162222	0.40	0.0230	17.19
GALNT3	ENSG00000115339	0.96	0.0560	17.16
NOP16	ENSG00000048162	0.73	0.0426	17.12
ENTPD6	ENSG00000197586	0.69	0.0405	17.08
RABGGTB	ENSG00000137955	0.50	0.0294	17.07
EMC9	ENSG00000100908	0.55	0.0321	17.05
KIT	ENSG00000157404	3.93	0.2308	17.03
TMX2	ENSG00000213593	0.45	0.0264	16.98
TFPI	ENSG00000003436	0.78	0.0459	16.94
PTPRQ	ENSG00000139304	3.49	0.2061	16.94
TIMM50	ENSG00000105197	0.38	0.0227	16.86
HIST1H2BK	ENSG00000197903	0.51	0.0306	16.78
FAM129B	ENSG00000136830	0.43	0.0264	16.46
MRPS11	ENSG00000181991	0.41	0.0252	16.44
KIAA0586	ENSG00000100578	0.46	0.0283	16.44
S100A3	ENSG00000188015	1.67	0.1018	16.43
KBTBD6	ENSG00000165572	0.47	0.0288	16.33

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TUBG1	ENSG00000131462	0.68	0.0420	16.31
MYPN	ENSG00000138347	2.05	0.1260	16.28
SLC44A2	ENSG00000129353	0.43	0.0267	16.24
PGK1	ENSG00000102144	0.63	0.0385	16.22
SH3BP4	ENSG00000130147	0.76	0.0469	16.20
ATP5G1	ENSG00000159199	0.57	0.0353	16.12
TNNT2	ENSG00000118194	0.83	0.0518	16.09
PSMD14	ENSG00000115233	0.51	0.0319	16.09
TNFAIP8L1	ENSG00000185361	1.00	0.0622	16.05
CISD3	ENSG00000230055	0.66	0.0412	15.98
SIGLEC11	ENSG00000269179	0.58	0.0363	15.97
GAS2L3	ENSG00000139354	1.02	0.0642	15.96
PLEKHB2	ENSG00000115762	0.49	0.0307	15.95
NUAK2	ENSG00000163545	2.03	0.1282	15.84
MPDU1	ENSG00000129255	0.41	0.0262	15.78
RP11-490H24.5	ENSG00000216285	0.58	0.0369	15.75
GLRX	ENSG00000173221	0.60	0.0383	15.74
CTD-2207O23.3	ENSG00000268861	0.73	0.0462	15.71
OSBPL3	ENSG00000070882	2.29	0.1458	15.71
ABCF2	ENSG00000033050	0.43	0.0273	15.70
PHF5A	ENSG00000100410	0.46	0.0294	15.70
TAGLN2	ENSG00000158710	0.77	0.0489	15.70
BRI3	ENSG00000164713	0.74	0.0474	15.70
UCHL5	ENSG00000116750	0.59	0.0377	15.69
RAD23B	ENSG00000119318	0.69	0.0441	15.61
EVI5L	ENSG00000142459	0.38	0.0245	15.60
ADK	ENSG00000156110	0.78	0.0501	15.59
AGK	ENSG00000006530	0.43	0.0277	15.59
EZH2	ENSG00000106462	0.50	0.0319	15.53
ZC3HC1	ENSG00000091732	0.39	0.0249	15.52
CDCA3	ENSG00000111665	1.26	0.0816	15.47
DDA1	ENSG00000130311	0.64	0.0414	15.42
VARS	ENSG00000204394	0.68	0.0441	15.40
NARS2	ENSG00000137513	0.38	0.0249	15.40
PGAM5	ENSG00000247077	0.65	0.0428	15.29
RALA	ENSG00000006451	0.38	0.0250	15.28
BOLA3	ENSG00000163170	0.64	0.0422	15.25
FAM3C2	ENSG00000174028	0.67	0.0440	15.24
PAPSS2	ENSG00000198682	2.07	0.1367	15.15
EHD2	ENSG00000024422	0.61	0.0405	15.12
ZHX3	ENSG00000174306	0.60	0.0396	15.10
SLC7A1	ENSG00000139514	0.76	0.0504	15.05
RAN	ENSG00000132341	0.71	0.0474	14.98
KLHL21	ENSG00000162413	0.52	0.0350	14.88
ATG3	ENSG00000144848	0.51	0.0342	14.87
DKFZP547B0914	ENSG00000269922	0.48	0.0325	14.84

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C1QBP	ENSG00000108561	0.53	0.0358	14.84
MRPL15	ENSG00000137547	0.44	0.0296	14.76
ANAPC15	ENSG00000110200	0.61	0.0414	14.75
CCDC138	ENSG00000163006	0.43	0.0289	14.75
PALM2-AKAP2	ENSG00000157654	0.43	0.0289	14.73
NRD1	ENSG00000078618	0.55	0.0373	14.70
RAD23BP1	ENSG00000236570	0.56	0.0384	14.67
SLC9A3R2	ENSG00000065054	0.93	0.0634	14.63
RAB3B	ENSG00000169213	1.43	0.0981	14.60
DEPDC1	ENSG00000024526	1.24	0.0853	14.59
GCNT4	ENSG00000176928	3.45	0.2367	14.59
RGMB	ENSG00000174136	1.49	0.1019	14.58
EFTUD1	ENSG00000140598	0.42	0.0287	14.58
PSMB3	ENSG00000108294	0.41	0.0284	14.56
ITGA7	ENSG00000135424	1.66	0.1141	14.54
ZC3H7B	ENSG00000100403	0.44	0.0300	14.53
DCXR	ENSG00000169738	0.55	0.0376	14.51
NDUFAF2	ENSG00000164182	0.39	0.0270	14.50
PHLDA3	ENSG00000174307	0.61	0.0419	14.49
KALRN	ENSG00000160145	2.52	0.1746	14.45
PTRF	ENSG00000177469	0.75	0.0518	14.43
LIPE	ENSG00000079435	0.96	0.0663	14.41
TACO1	ENSG00000136463	0.56	0.0386	14.41
PPIL1	ENSG00000137168	0.59	0.0411	14.37
POLE4	ENSG00000115350	0.50	0.0347	14.37
PNO1	ENSG00000115946	0.50	0.0347	14.37
MAD2L1	ENSG00000164109	0.95	0.0663	14.33
PA2G4P4	ENSG00000230457	0.75	0.0523	14.28
PSENEN	ENSG00000205155	0.48	0.0339	14.24
PTPLB	ENSG00000206527	0.78	0.0545	14.24
YWHAE	ENSG00000108953	0.40	0.0279	14.15
AP001258.4	ENSG00000245571	1.12	0.0794	14.15
PEA15	ENSG00000162734	0.86	0.0606	14.13
MAD2L2	ENSG00000116670	0.45	0.0319	14.10
JPH2	ENSG00000149596	1.41	0.0999	14.09
EMC6	ENSG00000127774	0.59	0.0422	14.03
STARD13	ENSG00000133121	0.81	0.0576	14.03
ELOVL7	ENSG00000164181	5.21	0.3713	14.03
RP6-109B7.3	ENSG00000241990	1.12	0.0802	14.01
TOMM40	ENSG00000130204	0.71	0.0505	14.00
APITD1-CORT	ENSG00000251503	0.43	0.0306	13.97
SNTB1	ENSG00000172164	1.21	0.0867	13.95
ATP8B1	ENSG00000081923	0.92	0.0662	13.94
CDK7	ENSG00000134058	0.39	0.0279	13.92
GDAP2	ENSG00000196505	0.39	0.0282	13.92
UQCRFS1	ENSG00000169021	0.42	0.0303	13.92

List of genes upregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

RP11-288D9.1	ENSG00000257424	3.24	0.2331	13.91
BTBD3	ENSG00000132640	0.61	0.0442	13.90
TRAK1	ENSG00000182606	0.66	0.0472	13.87
COX20	ENSG00000203667	0.60	0.0435	13.86
ZNF880	ENSG00000221923	1.43	0.1037	13.79
SRGAP2B	ENSG00000196369	0.41	0.0300	13.77
FAM3C	ENSG00000196937	0.71	0.0517	13.75
ARMC7	ENSG00000125449	0.53	0.0388	13.73
SNRPD3	ENSG00000100028	0.42	0.0303	13.72
PKP4	ENSG00000144283	0.99	0.0723	13.71
CXorf38	ENSG00000185753	0.50	0.0364	13.69
BCCIP	ENSG00000107949	0.49	0.0359	13.59
FRMD6	ENSG00000139926	0.89	0.0652	13.59
CRYBB2P1	ENSG00000100058	0.41	0.0301	13.56
ACO1	ENSG00000122729	0.48	0.0358	13.53
PHB	ENSG00000167085	0.44	0.0324	13.49
MAFG-AS1	ENSG00000265688	0.62	0.0459	13.49
PFKP	ENSG00000067057	0.42	0.0313	13.48
TNPO1	ENSG00000083312	0.57	0.0427	13.45
LINC00467	ENSG00000153363	0.91	0.0675	13.44
ANK1	ENSG00000029534	0.93	0.0691	13.42
LOXL2	ENSG00000134013	1.93	0.1435	13.42
RAC1P2	ENSG00000249936	0.45	0.0335	13.42
GAPDHP60	ENSG00000248180	0.64	0.0480	13.42
HN1	ENSG00000189159	0.67	0.0500	13.38
CDC20P1	ENSG00000231007	1.52	0.1133	13.38
AIFM2	ENSG00000042286	0.69	0.0516	13.37
NOP14-AS1	ENSG00000249673	0.50	0.0371	13.36
DLGAP5	ENSG00000126787	1.25	0.0938	13.35
WDR92	ENSG00000243667	0.40	0.0301	13.34
CTDSPL	ENSG00000144677	0.70	0.0523	13.34
CXCL1	ENSG00000163739	1.34	0.1008	13.33
ABCA11P	ENSG00000251595	0.49	0.0373	13.22
MOSPD2	ENSG00000130150	1.12	0.0850	13.22
UBASH3B	ENSG00000154127	0.57	0.0431	13.21
TNC	ENSG00000041982	1.38	0.1044	13.21
EPS8L2	ENSG00000177106	0.90	0.0684	13.20
TMEM97	ENSG00000109084	2.25	0.1712	13.16
GPN1	ENSG00000198522	0.41	0.0314	13.16
RNF145	ENSG00000145860	0.43	0.0330	13.11
HSPD1	ENSG00000144381	0.45	0.0347	13.09
DBF4B	ENSG00000161692	0.75	0.0574	13.08
RP11-879F14.2	ENSG00000267279	1.67	0.1276	13.07
ABT1	ENSG00000146109	0.45	0.0342	13.07
MRPS36	ENSG00000134056	0.56	0.0428	13.05
CCNA2	ENSG00000145386	1.17	0.0901	12.98

List of genes upregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

RP3-406P24.1	ENSG00000216657	0.54	0.0415	12.97
CCT4	ENSG00000115484	0.38	0.0297	12.88
TOMM6	ENSG00000214736	0.38	0.0300	12.84
PPA1	ENSG00000180817	0.52	0.0403	12.83
MCTS1	ENSG00000232119	0.63	0.0488	12.83
PPP1CC	ENSG00000186298	0.46	0.0361	12.83
TAF9	ENSG00000085231	0.54	0.0424	12.82
CLPP	ENSG00000125656	0.52	0.0404	12.81
ARF6	ENSG00000165527	0.57	0.0446	12.80
EMG1	ENSG00000126749	0.57	0.0448	12.79
CCT8	ENSG00000156261	0.44	0.0348	12.75
SBDSP1	ENSG00000225648	0.40	0.0313	12.74
PRR13	ENSG00000205352	0.51	0.0399	12.74
CTD-2302E22.3	ENSG00000258645	1.26	0.0986	12.74
JRK	ENSG00000234616	0.50	0.0394	12.73
RP11-77I22.3	ENSG00000235884	0.63	0.0495	12.72
MNF1	ENSG00000137288	0.39	0.0309	12.64
CDCA7L	ENSG00000164649	2.05	0.1620	12.64
CSTF2	ENSG00000101811	0.54	0.0429	12.62
TSSC1	ENSG00000032389	0.55	0.0439	12.62
GLRX2	ENSG00000023572	0.97	0.0768	12.62
C11orf68	ENSG00000175573	0.44	0.0347	12.62
IPO5	ENSG00000065150	0.54	0.0425	12.61
FAM72B	ENSG00000188610	1.32	0.1046	12.60
PADI1	ENSG00000142623	1.68	0.1332	12.60
STOM	ENSG00000148175	0.80	0.0634	12.56
DPH2	ENSG00000132768	0.59	0.0466	12.56
NRG1	ENSG00000157168	4.70	0.3747	12.54
CHEK2	ENSG00000183765	0.77	0.0613	12.53
RAC3	ENSG00000169750	0.51	0.0407	12.51
SOX13	ENSG00000143842	1.61	0.1290	12.50
KIAA1161	ENSG00000164976	0.59	0.0475	12.46
LLGL2	ENSG00000073350	0.76	0.0607	12.44
SMIM12	ENSG00000163866	0.53	0.0423	12.44
RP11-490M8.1	ENSG00000260025	1.13	0.0915	12.40
NDUFV2P1	ENSG00000267809	0.60	0.0488	12.37
ALDOC	ENSG00000109107	0.55	0.0449	12.35
CDK2AP2	ENSG00000167797	0.56	0.0455	12.33
TOX	ENSG00000198846	1.64	0.1335	12.27
NME7	ENSG00000143156	0.70	0.0569	12.26
SNRPG	ENSG00000143977	0.51	0.0418	12.23
TEAD1	ENSG00000187079	0.58	0.0480	12.14
RANGAP1	ENSG00000100401	0.96	0.0789	12.13
CENPN	ENSG00000166451	0.90	0.0738	12.12
STXBP6	ENSG00000168952	3.12	0.2577	12.12
DNAJC7	ENSG00000168259	0.43	0.0354	12.11

List of genes upregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

QSOX1	ENSG00000116260	0.96	0.0792	12.10
RAB8A	ENSG00000167461	0.52	0.0432	12.02
PFN1	ENSG00000108518	0.78	0.0651	11.99
CCDC51	ENSG00000164051	0.85	0.0712	11.99
AMOTL2	ENSG00000114019	0.68	0.0569	11.99
CKAP2	ENSG00000136108	0.85	0.0711	11.95
C19orf25	ENSG00000119559	0.66	0.0554	11.93
CENPE	ENSG00000138778	1.32	0.1106	11.93
USP39	ENSG00000168883	0.45	0.0374	11.93
STC2	ENSG00000113739	0.38	0.0320	11.91
AJUBA	ENSG00000129474	0.72	0.0604	11.89
SKA2	ENSG00000182628	0.77	0.0652	11.84
RRS1	ENSG00000179041	0.99	0.0837	11.82
TAF1D	ENSG00000166012	0.44	0.0371	11.81
MYRIP	ENSG00000170011	3.46	0.2929	11.81
CARS2	ENSG00000134905	0.52	0.0442	11.79
LSM4	ENSG00000130520	0.86	0.0731	11.76
OCLN	ENSG00000197822	1.00	0.0847	11.76
GNG12	ENSG00000172380	0.52	0.0442	11.74
FYN	ENSG00000010810	0.94	0.0804	11.71
IP6K3	ENSG00000161896	2.05	0.1754	11.71
NDUFS6	ENSG00000145494	0.51	0.0438	11.70
CBX1	ENSG00000108468	0.44	0.0375	11.70
RPA3	ENSG00000106399	0.77	0.0655	11.68
SCD5	ENSG00000145284	0.52	0.0444	11.68
ADA	ENSG00000196839	1.38	0.1184	11.67
RRP15	ENSG00000067533	0.51	0.0439	11.65
OARD1	ENSG00000124596	0.52	0.0447	11.65
EIF5A	ENSG00000132507	0.44	0.0375	11.64
HRAS	ENSG00000174775	0.60	0.0516	11.63
EXOSC8	ENSG00000120699	0.51	0.0440	11.62
FAM83G	ENSG00000188522	0.53	0.0454	11.61
CMC2	ENSG00000103121	0.53	0.0453	11.59
NEK2	ENSG00000117650	1.20	0.1033	11.58
MRPS24	ENSG00000062582	0.65	0.0565	11.54
FST	ENSG00000134363	2.01	0.1740	11.54
STK4	ENSG00000101109	0.47	0.0406	11.54

List of genes downregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

Gene Symbol	ENSEMBL ID	mean fold change	sd	Z score
GTF2IRD2B	ENSG00000174428	-1.34	0.0024	-545.53
NBL1	ENSG00000270136	-0.74	0.0022	-343.88
DNMT3A	ENSG00000119772	-1.31	0.0054	-241.91
ACADVL	ENSG00000072778	-0.69	0.0035	-196.03
FAM171A2	ENSG00000161682	-1.34	0.0115	-115.94
SAMD11	ENSG00000187634	-4.58	0.0453	-101.24
ZNF605	ENSG00000196458	-0.79	0.0085	-93.72
ABCA10	ENSG00000154263	-1.35	0.0152	-88.77
KLF3	ENSG00000109787	-0.93	0.0109	-85.14
RP11-96C23.11	ENSG00000261011	-1.78	0.0217	-82.18
PAQR8	ENSG00000170915	-1.36	0.0167	-81.79
ZNF713	ENSG00000178665	-2.12	0.0259	-81.79
MDM4	ENSG00000198625	-0.84	0.0116	-71.97
CDON	ENSG00000064309	-3.71	0.0532	-69.73
SLC44A1	ENSG00000070214	-0.74	0.0107	-69.46
DEAF1	ENSG00000177030	-0.54	0.0082	-66.14
ZMYM5	ENSG00000132950	-0.76	0.0119	-63.62
SETD5-AS1	ENSG00000206573	-0.48	0.0077	-62.63
KIAA1755	ENSG00000149633	-4.70	0.0755	-62.21
ANKH	ENSG00000154122	-2.94	0.0485	-60.70
ZNF836	ENSG00000196267	-0.77	0.0135	-57.27
ZNF333	ENSG00000160961	-0.66	0.0117	-56.98
CA11	ENSG00000063180	-2.28	0.0403	-56.68
MAFF	ENSG00000185022	-0.59	0.0105	-55.85
FAM155A	ENSG00000204442	-0.97	0.0175	-55.48
SMIM11	ENSG00000205670	-0.51	0.0092	-55.05
ZC2HC1A	ENSG00000104427	-0.67	0.0122	-54.69
KDM2A	ENSG00000173120	-0.45	0.0085	-52.53
CABLES1	ENSG00000134508	-1.92	0.0372	-51.65
DOCK4	ENSG00000128512	-1.32	0.0268	-49.38
DPY19L1	ENSG00000173852	-1.01	0.0208	-48.67
HERC2P9	ENSG00000206149	-0.45	0.0094	-47.58
CYHR1	ENSG00000187954	-0.47	0.0100	-47.13
TSPAN31	ENSG00000135452	-0.39	0.0085	-46.24
REV3L	ENSG00000009413	-0.72	0.0158	-45.61
PROS1	ENSG00000184500	-1.53	0.0335	-45.59
LRIG3	ENSG00000139263	-1.46	0.0335	-43.64
C7orf53	ENSG00000181016	-1.19	0.0280	-42.47
PAM	ENSG00000145730	-0.65	0.0159	-40.73
SH3GLB2	ENSG00000148341	-0.87	0.0217	-40.20
ATG16L2	ENSG00000168010	-1.14	0.0284	-40.12
UBE2F	ENSG00000258984	-0.40	0.0101	-39.78
GULP1	ENSG00000144366	-1.50	0.0382	-39.32

List of genes downregulated by merlin inactivation in the arachnoidal cell system as determined by Z-score in initial analyses in Y1 and Y2

PRSS3	ENSG00000010438	-0.71	0.0184	-38.86
CCNL1	ENSG00000163660	-0.73	0.0187	-38.79
SCN3A	ENSG00000153253	-3.60	0.0933	-38.59
NCOA1	ENSG00000084676	-0.53	0.0139	-38.46
AC005562.1	ENSG00000214719	-0.38	0.0102	-37.60
PGAP3	ENSG00000161395	-1.02	0.0272	-37.28
RNASEL	ENSG00000135828	-0.92	0.0248	-37.04
RASL11A	ENSG00000122035	-3.54	0.0960	-36.89
PI4KAP2	ENSG00000183506	-0.89	0.0247	-36.13
ATHL1	ENSG00000142102	-0.75	0.0208	-36.05
EGR2	ENSG00000122877	-3.10	0.0880	-35.27
GPC6	ENSG00000183098	-1.92	0.0548	-35.03
MBTD1	ENSG00000011258	-0.66	0.0196	-33.60
CREBRF	ENSG00000164463	-1.01	0.0303	-33.32
CTD-3247F14.2	ENSG00000261026	-4.46	0.1354	-32.95
TIMP1	ENSG00000102265	-0.46	0.0140	-32.78
CD302	ENSG00000241399	-1.39	0.0428	-32.52
MBTPS1	ENSG00000140943	-0.45	0.0142	-32.14
ZNF266	ENSG00000174652	-0.53	0.0166	-32.13
TMEM216	ENSG00000187049	-0.68	0.0214	-32.03
DDIT4L	ENSG00000145358	-2.97	0.0944	-31.48
CNTNAP3	ENSG00000106714	-2.89	0.0920	-31.43
SYNDIG1	ENSG00000101463	-2.92	0.0929	-31.40
DYNC2H1	ENSG00000187240	-0.52	0.0166	-31.25
FKBP7	ENSG00000079150	-0.92	0.0297	-30.83
DISP1	ENSG00000154309	-1.72	0.0560	-30.67
ELOVL5	ENSG00000012660	-0.60	0.0196	-30.43
RAB33B	ENSG00000172007	-0.73	0.0242	-30.19
GPR173	ENSG00000184194	-1.24	0.0412	-30.19
GOLGA6L5	ENSG00000230373	-1.24	0.0411	-30.10
HGSNAT	ENSG00000165102	-0.55	0.0187	-29.20
PCDH18	ENSG00000189184	-1.50	0.0518	-28.97
OSR1	ENSG00000143867	-1.07	0.0370	-28.79
MARCH8	ENSG00000165406	-0.47	0.0166	-28.43
DGKI	ENSG00000157680	-1.41	0.0496	-28.36
GPR125	ENSG00000152990	-0.73	0.0257	-28.32
ZMYM2	ENSG00000121741	-0.48	0.0171	-28.27
ADAMTS14	ENSG00000138316	-0.97	0.0346	-27.95
LPIN2	ENSG00000101577	-0.40	0.0145	-27.94
LAG3	ENSG00000089692	-1.86	0.0667	-27.82
GEM	ENSG00000164949	-1.12	0.0405	-27.74
KDM1B	ENSG00000165097	-0.88	0.0318	-27.65
RP11-1407O15.2	ENSG00000174093	-0.63	0.0230	-27.30
SLC38A2	ENSG00000134294	-1.24	0.0457	-27.16
LRP4	ENSG00000134569	-3.72	0.1391	-26.77

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CCDC120	ENSG00000147144	-1.25	0.0468	-26.72
PCDHB8	ENSG00000120322	-3.33	0.1255	-26.57
KIAA1683	ENSG00000130518	-2.68	0.1010	-26.49
ESYT2	ENSG00000117868	-0.64	0.0244	-26.34
PPAP2A	ENSG00000067113	-1.16	0.0442	-26.18
LTBP3	ENSG00000168056	-1.65	0.0630	-26.13
SMARCD3	ENSG00000082014	-1.38	0.0530	-26.05
PLXNA4	ENSG00000221866	-4.10	0.1576	-25.99
NSMF	ENSG00000165802	-1.45	0.0559	-25.89
DOCK5	ENSG00000147459	-0.38	0.0148	-25.78
GNB3	ENSG00000111664	-1.57	0.0610	-25.64
BOC	ENSG00000144857	-3.85	0.1501	-25.62
NEIL1	ENSG00000140398	-1.95	0.0769	-25.36
SOX4	ENSG00000124766	-3.29	0.1296	-25.36
DCN	ENSG00000011465	-1.27	0.0504	-25.12
KLF13	ENSG00000169926	-0.99	0.0396	-25.10
ATXN3	ENSG00000066427	-0.58	0.0233	-24.91
SIAH1	ENSG00000196470	-0.44	0.0181	-24.45
NIPAL2	ENSG00000104361	-1.52	0.0622	-24.41
YPEL3	ENSG00000090238	-1.12	0.0460	-24.32
SSR1	ENSG00000124783	-0.41	0.0168	-24.20
POU6F1	ENSG00000184271	-2.01	0.0834	-24.14
WSB1	ENSG00000109046	-0.89	0.0368	-24.07
SLC20A1	ENSG00000144136	-0.66	0.0275	-23.97
RAI2	ENSG00000131831	-4.87	0.2043	-23.86
SGSM2	ENSG00000141258	-0.66	0.0277	-23.85
ITGB8	ENSG00000105855	-3.97	0.1673	-23.70
TRIM62	ENSG00000116525	-1.77	0.0746	-23.68
CRTC3	ENSG00000140577	-0.62	0.0263	-23.35
RP11-875O11.1	ENSG00000245025	-1.04	0.0445	-23.30
MRC2	ENSG00000011028	-1.02	0.0441	-23.17
PDE4A	ENSG00000065989	-0.90	0.0387	-23.14
RUNX1	ENSG00000159216	-0.99	0.0427	-23.09
HDAC6	ENSG00000094631	-0.44	0.0189	-23.07
NUDT4	ENSG00000173598	-0.60	0.0262	-22.89
SH3BP2	ENSG00000087266	-0.74	0.0325	-22.86
RNF103	ENSG00000239305	-0.74	0.0324	-22.79
PHLDB2	ENSG00000144824	-0.63	0.0278	-22.59
TTLL3	ENSG00000214021	-1.84	0.0816	-22.57
S1PR2	ENSG00000267534	-1.03	0.0462	-22.34
SLC9A9	ENSG00000181804	-2.37	0.1067	-22.20
CCDC92	ENSG00000119242	-0.94	0.0426	-22.15
PEAK1	ENSG00000173517	-0.52	0.0237	-22.00
DHRS3	ENSG00000162496	-1.47	0.0669	-22.00
LGALS3	ENSG00000131981	-1.29	0.0584	-22.00
RBPJ	ENSG00000168214	-0.55	0.0253	-21.93

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RP11-159D12.2	ENSG00000264112	-0.73	0.0332	-21.87
ZNF117	ENSG00000152926	-1.70	0.0779	-21.85
RP11-274B21.2	ENSG00000243302	-0.64	0.0295	-21.72
TTBK2	ENSG00000128881	-0.78	0.0359	-21.66
PTTG1IP	ENSG00000183255	-0.38	0.0178	-21.62
L3MBTL1	ENSG00000185513	-1.10	0.0508	-21.61
BMPR2	ENSG00000204217	-0.39	0.0179	-21.57
AHCYL2	ENSG00000158467	-2.99	0.1393	-21.46
RP4-657D16.3	ENSG00000266993	-1.70	0.0792	-21.46
AUH	ENSG00000148090	-0.78	0.0362	-21.45
PLCL1	ENSG00000115896	-5.34	0.2490	-21.44
SESTD1	ENSG00000187231	-0.87	0.0406	-21.34
AAED1	ENSG00000158122	-0.67	0.0313	-21.26
RP4-773N10.4	ENSG00000258634	-0.63	0.0299	-21.11
MERTK	ENSG00000153208	-2.68	0.1272	-21.10
NCOA2	ENSG00000140396	-0.64	0.0303	-21.03
SIX5	ENSG00000177045	-0.56	0.0266	-21.01
KIAA0247	ENSG00000100647	-1.21	0.0579	-20.93
AKAP1	ENSG00000121057	-0.96	0.0461	-20.91
P4HTM	ENSG00000178467	-0.53	0.0256	-20.83
ARHGAP5	ENSG00000100852	-0.51	0.0246	-20.79
PKDCC	ENSG00000162878	-2.26	0.1086	-20.77
GRK5	ENSG00000198873	-1.23	0.0593	-20.75
PRRT2	ENSG00000167371	-1.61	0.0777	-20.68
YPEL1	ENSG00000100027	-4.59	0.2228	-20.59
FAM8A1	ENSG00000137414	-1.66	0.0808	-20.58
DMTF1	ENSG00000135164	-0.47	0.0230	-20.40
GBA2	ENSG00000070610	-0.42	0.0206	-20.29
THOC6	ENSG00000131652	-1.25	0.0619	-20.26
ATP6V0E2-AS1	ENSG00000204934	-0.58	0.0286	-20.25
AKR7L	ENSG00000211454	-1.52	0.0750	-20.22
RAB27B	ENSG00000041353	-1.35	0.0672	-20.07
PIAS2	ENSG00000078043	-0.52	0.0261	-20.04
DTNB	ENSG00000138101	-1.40	0.0703	-19.95
CCDC159	ENSG00000183401	-1.48	0.0742	-19.92
TPT1-AS1	ENSG00000170919	-0.99	0.0499	-19.85
RRAGB	ENSG00000083750	-0.82	0.0413	-19.78
PPFIBP1	ENSG00000110841	-2.50	0.1264	-19.77
ICA1L	ENSG00000163596	-1.60	0.0813	-19.72
TDRD3	ENSG00000083544	-0.40	0.0202	-19.66
GFPT2	ENSG00000131459	-1.79	0.0919	-19.52
WASL	ENSG00000106299	-0.62	0.0318	-19.48
CFLAR	ENSG00000003402	-0.45	0.0231	-19.41
TNRC6B	ENSG00000100354	-0.60	0.0309	-19.41
CTDSP2	ENSG00000175215	-0.49	0.0252	-19.40
ZNF445	ENSG00000185219	-0.57	0.0292	-19.39

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ZCCHC14	ENSG00000140948	-1.49	0.0771	-19.33
EVC	ENSG00000072840	-0.62	0.0323	-19.26
VPS13C	ENSG00000129003	-0.56	0.0291	-19.19
AKAP9	ENSG00000127914	-0.58	0.0303	-19.09
MAPK1	ENSG00000100030	-0.43	0.0224	-19.03
PCDHB6	ENSG00000113211	-1.96	0.1029	-19.03
CCNB1IP1	ENSG00000100814	-0.48	0.0252	-18.97
RP11-815I9.4	ENSG00000264885	-0.82	0.0435	-18.93
GPR1	ENSG00000183671	-0.69	0.0369	-18.80
WWTR1	ENSG00000018408	-0.97	0.0516	-18.79
ZNF32	ENSG00000169740	-0.54	0.0286	-18.76
FBXL17	ENSG00000145743	-0.49	0.0261	-18.64
DIXDC1	ENSG00000150764	-1.24	0.0667	-18.59
TP53I3	ENSG00000115129	-0.52	0.0280	-18.58
GRN	ENSG00000030582	-0.55	0.0299	-18.43
ZBTB14	ENSG00000198081	-0.51	0.0277	-18.36
ZNF10	ENSG00000256223	-1.04	0.0566	-18.36
AF131215.9	ENSG00000269918	-0.93	0.0508	-18.35
NISCH	ENSG00000010322	-0.57	0.0312	-18.29
FAM89B	ENSG00000176973	-0.76	0.0417	-18.27
LPP	ENSG00000145012	-0.52	0.0286	-18.26
ERV3-1	ENSG00000213462	-1.30	0.0711	-18.26
WDR60	ENSG00000126870	-0.46	0.0256	-18.10
TTC3	ENSG00000182670	-0.80	0.0444	-18.02
DNAH10OS	ENSG00000250091	-2.06	0.1145	-17.98
RP11-54O7.3	ENSG00000223764	-3.35	0.1871	-17.88
C14orf159	ENSG00000133943	-2.12	0.1186	-17.86
OS9	ENSG00000135506	-0.43	0.0240	-17.84
PRRX1	ENSG00000116132	-0.80	0.0452	-17.78
VPS13A	ENSG00000197969	-0.40	0.0228	-17.67
CTSA	ENSG00000064601	-0.73	0.0416	-17.63
ARMC9	ENSG00000135931	-1.40	0.0799	-17.57
KDM3A	ENSG00000115548	-0.79	0.0448	-17.54
INSR	ENSG00000171105	-1.07	0.0614	-17.49
FYCO1	ENSG00000163820	-0.93	0.0533	-17.47
ZNF573	ENSG00000189144	-0.45	0.0257	-17.45
MEIS3	ENSG00000105419	-0.46	0.0264	-17.41
N4BP2L1	ENSG00000139597	-2.61	0.1505	-17.37
MGAT4B	ENSG00000161013	-0.64	0.0369	-17.35
PLK3	ENSG00000173846	-0.66	0.0382	-17.32
STIM2	ENSG00000109689	-0.72	0.0418	-17.26
CTD-2545G14.7	ENSG00000262526	-0.39	0.0229	-17.23
PLEKHA4	ENSG00000105559	-0.99	0.0579	-17.19
ZNF425	ENSG00000204947	-0.79	0.0458	-17.18
PTPRU	ENSG00000060656	-3.57	0.2084	-17.11
TRIM52	ENSG00000183718	-0.53	0.0312	-17.10

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DNAJC18	ENSG00000170464	-0.62	0.0362	-17.07
ZNF444	ENSG00000167685	-0.38	0.0223	-17.04
SOS2	ENSG00000100485	-0.45	0.0264	-16.99
IQCH-AS1	ENSG00000259673	-1.19	0.0700	-16.99
AC005863.1	ENSG00000205325	-0.93	0.0548	-16.92
ID2	ENSG00000115738	-0.72	0.0429	-16.89
TEN1-CDK3	ENSG00000261408	-0.45	0.0266	-16.86
NR2C1	ENSG00000120798	-0.61	0.0364	-16.85
RP11-539L10.3	ENSG00000251580	-1.16	0.0689	-16.83
AMER1	ENSG00000184675	-0.54	0.0323	-16.76
KIAA2018	ENSG00000176542	-0.44	0.0265	-16.72
RP11-292B8.1	ENSG00000215142	-1.58	0.0946	-16.67
CTSF	ENSG00000174080	-1.86	0.1117	-16.62
RGL2	ENSG00000237441	-0.66	0.0396	-16.58
ANKRD44	ENSG00000065413	-1.19	0.0721	-16.55
CHMP1B	ENSG00000255112	-0.93	0.0560	-16.51
TMEM198B	ENSG00000182796	-1.08	0.0652	-16.51
PCDHB11	ENSG00000197479	-3.67	0.2227	-16.49
GPX4	ENSG00000167468	-0.48	0.0291	-16.39
GAS1	ENSG00000180447	-4.31	0.2628	-16.38
ZBTB10	ENSG00000205189	-0.69	0.0424	-16.36
LENG8	ENSG00000167615	-1.12	0.0687	-16.36
INADL	ENSG00000132849	-0.92	0.0562	-16.34
ZFAND5	ENSG00000107372	-0.93	0.0567	-16.31
IL11RA	ENSG00000137070	-0.44	0.0269	-16.30
BACE1	ENSG00000186318	-0.87	0.0534	-16.27
BACE1	ENSG00000265969	-0.70	0.0428	-16.26
SYNGAP1	ENSG00000197283	-0.88	0.0546	-16.19
LINC00174	ENSG00000179406	-1.15	0.0711	-16.17
GABRE	ENSG00000102287	-1.13	0.0699	-16.15
ZNF30	ENSG00000168661	-0.62	0.0388	-16.04
LTBP2	ENSG00000119681	-2.46	0.1539	-15.99
RAMP1	ENSG00000132329	-2.59	0.1625	-15.95
UBE2F	ENSG00000184182	-0.58	0.0362	-15.94
RNF130	ENSG00000113269	-0.88	0.0552	-15.92
KIAA2026	ENSG00000183354	-0.39	0.0243	-15.92
HECTD4	ENSG00000173064	-0.71	0.0450	-15.74
GLIS2	ENSG00000126603	-0.67	0.0427	-15.73
RHOBTB3	ENSG00000164292	-0.49	0.0313	-15.70
NAMPT	ENSG00000105835	-0.77	0.0492	-15.64
RP4-798P15.3	ENSG00000254154	-0.71	0.0456	-15.63
LRP1	ENSG00000123384	-1.03	0.0661	-15.63
PAPSS1	ENSG00000138801	-0.66	0.0422	-15.55
ABR	ENSG00000159842	-0.56	0.0359	-15.52
TCTN1	ENSG00000204852	-0.86	0.0555	-15.45
TRPS1	ENSG00000104447	-0.99	0.0641	-15.39

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DIRAS1	ENSG00000176490	-2.58	0.1679	-15.37
ZNF345	ENSG00000251247	-1.08	0.0702	-15.37
LY75	ENSG00000054219	-1.39	0.0907	-15.37
SCUBE3	ENSG00000146197	-0.96	0.0623	-15.33
C1orf233	ENSG00000228594	-0.51	0.0335	-15.31
RP11-252A24.7	ENSG00000260539	-0.88	0.0572	-15.31
ARID2	ENSG00000189079	-0.59	0.0387	-15.30
KRT10	ENSG00000186395	-0.38	0.0248	-15.30
SNX9	ENSG00000130340	-1.00	0.0653	-15.27
ZBTB48	ENSG00000204859	-0.42	0.0276	-15.24
PCED1A	ENSG00000132635	-0.48	0.0315	-15.24
RP11-396K3.1	ENSG00000233369	-1.15	0.0756	-15.22
C16orf45	ENSG00000166780	-0.77	0.0510	-15.19
RP13-507I23.1	ENSG00000235703	-1.58	0.1040	-15.19
CTC-273B12.8	ENSG00000269751	-0.80	0.0528	-15.09
TRIM13	ENSG00000204977	-0.51	0.0339	-15.06
PLD2	ENSG00000129219	-0.67	0.0448	-15.05
ZNF529	ENSG00000186020	-0.70	0.0469	-15.02
TMTC4	ENSG00000125247	-1.36	0.0907	-15.00
SSBP3	ENSG00000157216	-1.09	0.0727	-14.99
TUBGCP6	ENSG00000128159	-0.53	0.0353	-14.95
CLDN15	ENSG00000106404	-0.92	0.0618	-14.94
ZNF470	ENSG00000197016	-0.65	0.0436	-14.93
LAMB1	ENSG00000091136	-0.72	0.0484	-14.92
PER3	ENSG00000049246	-1.14	0.0769	-14.83
ZNF184	ENSG00000096654	-0.73	0.0497	-14.76
ITPR2	ENSG00000123104	-0.97	0.0658	-14.74
ARSB	ENSG00000113273	-1.01	0.0685	-14.72
ADCY6	ENSG00000174233	-0.56	0.0380	-14.70
ZMYM6	ENSG00000163867	-0.42	0.0283	-14.69
GLT8D2	ENSG00000120820	-1.65	0.1125	-14.66
MLLT6	ENSG00000108292	-0.51	0.0353	-14.54
ELF1	ENSG00000120690	-0.44	0.0301	-14.52
EML3	ENSG00000149499	-0.40	0.0279	-14.46
HCFC1R1	ENSG00000103145	-1.45	0.1009	-14.40
RP1-261D10.2	ENSG00000259146	-1.82	0.1265	-14.35
DYRK1B	ENSG00000105204	-0.61	0.0427	-14.35
ZNF133	ENSG00000125846	-0.50	0.0350	-14.20
ARHGEF40	ENSG00000165801	-0.86	0.0609	-14.18
CAMLG	ENSG00000164615	-0.60	0.0425	-14.15
LY75-CD302	ENSG00000248672	-1.37	0.0972	-14.04
ARRDC3	ENSG00000113369	-1.51	0.1078	-14.03
LTBP4	ENSG00000090006	-1.32	0.0945	-14.02
BAG2	ENSG00000112208	-0.74	0.0526	-14.01
PI4KAP1	ENSG00000215513	-0.77	0.0554	-13.99
MVB12B	ENSG00000196814	-0.87	0.0623	-13.95

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SEPP1	ENSG00000250722	-7.09	0.5079	-13.95
CRY2	ENSG00000121671	-0.70	0.0500	-13.95
MAP3K14	ENSG00000006062	-0.43	0.0307	-13.93
ZNF805	ENSG00000204524	-1.06	0.0758	-13.93
CPD	ENSG00000108582	-0.52	0.0376	-13.86
NFIL3	ENSG00000165030	-1.34	0.0971	-13.84
CTC-203F4.1	ENSG00000224186	-1.40	0.1009	-13.84
SUMF1	ENSG00000144455	-0.51	0.0367	-13.84
KDM6B	ENSG00000132510	-1.45	0.1049	-13.83
TCF25	ENSG00000141002	-0.43	0.0311	-13.82
SCLY	ENSG00000132330	-0.39	0.0284	-13.81
AC007283.5	ENSG00000234431	-0.68	0.0495	-13.81
RP11-196G11.4	ENSG00000262766	-0.85	0.0616	-13.81
C3orf62	ENSG00000188315	-1.10	0.0798	-13.77
PHYH	ENSG00000107537	-0.75	0.0547	-13.76
ABCA8	ENSG00000141338	-2.30	0.1676	-13.73
CTD-2339L15.1	ENSG00000245849	-0.78	0.0566	-13.71
ZFHX3	ENSG00000140836	-0.66	0.0482	-13.68
MARC2	ENSG00000117791	-0.42	0.0307	-13.68
CTC-444N24.8	ENSG00000268713	-1.45	0.1057	-13.67
SH3BP5-AS1	ENSG00000224660	-1.35	0.0988	-13.61
BAZ2B	ENSG00000123636	-1.21	0.0891	-13.61
RP11-469M7.1	ENSG00000260006	-1.48	0.1092	-13.58
AMH	ENSG00000104899	-0.73	0.0537	-13.57
PLEKHA7	ENSG00000166689	-5.17	0.3823	-13.52
PCMTD1	ENSG00000168300	-1.23	0.0908	-13.51
MAN2B1	ENSG00000104774	-0.57	0.0419	-13.49
TRPC1	ENSG00000144935	-0.77	0.0571	-13.46
TSHZ3	ENSG00000121297	-0.45	0.0338	-13.43
FAM131B	ENSG00000159784	-1.58	0.1180	-13.42
LUM	ENSG00000139329	-1.44	0.1070	-13.41
PPP3CA	ENSG00000138814	-0.96	0.0713	-13.41
RP11-181G12.2	ENSG00000182873	-0.70	0.0524	-13.40
PCDHB14	ENSG00000120327	-2.62	0.1971	-13.30
ST6GALNAC2	ENSG00000070731	-3.19	0.2399	-13.29
FAM229A	ENSG00000225828	-1.34	0.1010	-13.28
CUTC	ENSG00000119929	-0.42	0.0316	-13.28
FER1L4	ENSG00000088340	-1.91	0.1443	-13.25
PPP1R12B	ENSG00000077157	-0.57	0.0429	-13.24
PTK7	ENSG00000112655	-0.66	0.0499	-13.21
RUFY3	ENSG00000018189	-0.83	0.0632	-13.18
SPHAR	ENSG00000213029	-0.59	0.0446	-13.14
ZMIZ1	ENSG00000108175	-0.80	0.0607	-13.14
GINM1	ENSG00000055211	-0.41	0.0316	-13.12
LRP10	ENSG00000197324	-0.44	0.0334	-13.07
ZNF224	ENSG00000267680	-0.59	0.0450	-13.06

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DUSP22	ENSG00000112679	-0.55	0.0420	-13.06
ETS2	ENSG00000157557	-0.89	0.0681	-13.03
MTMR11	ENSG00000014914	-0.69	0.0531	-13.02
ZNF250	ENSG00000196150	-0.61	0.0467	-13.02
SOS1	ENSG00000115904	-0.42	0.0322	-13.02
RBBP6	ENSG00000122257	-0.39	0.0297	-13.01
ADAMTS13	ENSG00000160323	-1.84	0.1419	-12.96
CDK19	ENSG00000155111	-0.66	0.0508	-12.92
GNL1	ENSG00000204590	-0.79	0.0615	-12.90
PCMTD2	ENSG00000203880	-0.81	0.0629	-12.90
FHL1	ENSG00000022267	-0.39	0.0301	-12.87
ABCD4	ENSG00000119688	-0.76	0.0595	-12.84
CEP68	ENSG00000011523	-0.71	0.0552	-12.83
C5orf4	ENSG00000170271	-1.80	0.1405	-12.83
WWOX	ENSG00000186153	-0.92	0.0716	-12.83
CTD-2535L24.2	ENSG00000266076	-1.05	0.0819	-12.81
WDR19	ENSG00000157796	-0.89	0.0697	-12.79
QRICH2	ENSG00000129646	-1.95	0.1526	-12.78
MEGF8	ENSG00000105429	-0.49	0.0387	-12.77
C20orf112	ENSG00000197183	-0.73	0.0571	-12.74
ZNF354B	ENSG00000178338	-0.47	0.0369	-12.72
DMXL1	ENSG00000172869	-0.38	0.0303	-12.64
TMEM64	ENSG00000180694	-0.72	0.0567	-12.64
RNF44	ENSG00000146083	-0.89	0.0706	-12.63
ZNF446	ENSG00000083838	-0.42	0.0330	-12.60
EGR3	ENSG00000179388	-2.78	0.2209	-12.59
LXN	ENSG00000079257	-1.45	0.1148	-12.59
FZD4	ENSG00000174804	-0.43	0.0341	-12.59
COL4A4	ENSG00000081052	-5.36	0.4262	-12.58
ABLIM1	ENSG00000099204	-1.65	0.1317	-12.55
ALDH3A2	ENSG00000072210	-1.30	0.1041	-12.53
DENND6A	ENSG00000174839	-0.44	0.0354	-12.51
CD47	ENSG00000196776	-0.44	0.0352	-12.49
THRA	ENSG00000126351	-0.94	0.0754	-12.49
RP11-20G6.3	ENSG00000260566	-0.86	0.0687	-12.47
DIAPH2	ENSG00000147202	-0.48	0.0385	-12.47
FAM171A1	ENSG00000148468	-0.50	0.0400	-12.45
TMEM132D	ENSG00000151952	-0.74	0.0594	-12.41
KBTBD3	ENSG00000182359	-0.39	0.0311	-12.40
PGM2L1	ENSG00000165434	-1.65	0.1331	-12.40
TGFB3	ENSG00000119699	-2.91	0.2352	-12.38
TGFB1	ENSG00000105329	-0.58	0.0469	-12.37
FHDC1	ENSG00000137460	-1.44	0.1169	-12.35
IFT80	ENSG00000068885	-0.68	0.0552	-12.27
KIAA1147	ENSG00000257093	-0.71	0.0578	-12.27
FN1	ENSG00000115414	-1.35	0.1101	-12.27

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ZNF503	ENSG00000165655	-1.69	0.1379	-12.27
PER2	ENSG00000132326	-2.28	0.1868	-12.21
PPAP2B	ENSG00000162407	-1.33	0.1092	-12.19
HSF4	ENSG00000102878	-1.32	0.1087	-12.17
WNT9A	ENSG00000143816	-2.05	0.1686	-12.14
ERRFI1	ENSG00000116285	-3.01	0.2480	-12.14
CBFA2T2	ENSG00000078699	-0.61	0.0507	-12.1
MEF2D	ENSG00000116604	-0.82	0.0673	-12.1
HECA	ENSG00000112406	-0.89	0.0736	-12.0
POGZ	ENSG00000143442	-0.42	0.0347	-12.0
RP11-603J24.7	ENSG00000237493	-0.71	0.0592	-12.0
ARL5B	ENSG00000165997	-0.70	0.0585	-12.0
RABL5	ENSG00000128581	-0.45	0.0373	-12.0
IDS	ENSG00000010404	-0.41	0.0341	-11.9
HINT3	ENSG00000111911	-0.38	0.0322	-11.9
CCNI	ENSG00000118816	-0.49	0.0411	-11.8
CAPS2	ENSG00000180881	-0.47	0.0398	-11.8
EEF2K	ENSG00000103319	-0.98	0.0823	-11.8
ITPRIP	ENSG00000148841	-0.95	0.0798	-11.8
GARNL3	ENSG00000136895	-1.28	0.1083	-11.8
CTD-2587M2.1	ENSG00000249476	-0.91	0.0769	-11.8
TBC1D3	ENSG00000197681	-0.82	0.0690	-11.8
HDAC4	ENSG00000068024	-0.66	0.0555	-11.8
CHD6	ENSG00000124177	-0.44	0.0371	-11.8
NCOA7	ENSG00000111912	-1.04	0.0883	-11.7
SLC23A2	ENSG00000089057	-0.63	0.0534	-11.7
CTSO	ENSG00000256043	-2.03	0.1732	-11.7
APOE	ENSG00000130203	-3.01	0.2574	-11.6
RP11-448G15.3	ENSG00000261490	-1.15	0.0982	-11.6
PLAGL1	ENSG00000118495	-0.96	0.0828	-11.6
AL163636.6	ENSG00000259171	-1.39	0.1198	-11.6
ZNF561	ENSG00000171469	-0.54	0.0464	-11.6
GALT	ENSG00000213930	-0.55	0.0470	-11.6
EFHC1	ENSG00000096093	-0.67	0.0581	-11.6
NPEPL1	ENSG00000215440	-0.39	0.0337	-11.6
MOXD1	ENSG00000079931	-0.87	0.0753	-11.5
TNFRSF25	ENSG00000215788	-1.11	0.0962	-11.5
KLF11	ENSG00000172059	-1.02	0.0883	-11.5

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

Gene Symbol	ENSEMBL ID	mean fold change	sd	Z score
OSBPL1A	ENSG00000141447	10.17	0.44	23.13
SLC15A3	ENSG00000110446	11.03	0.63	17.62
COL6A2	ENSG00000142173	10.46	0.60	17.34
PHYHD1	ENSG00000175287	8.80	0.53	16.66
PARP11	ENSG00000111224	6.79	0.42	16.10
TCF7L1	ENSG00000152284	7.60	0.47	16.05
FAM127C	ENSG00000212747	5.26	0.35	15.08
MYH10	ENSG00000133026	12.39	0.87	14.30
LARGE	ENSG00000133424	6.94	0.54	12.96
CASP4	ENSG00000196954	6.90	0.54	12.88
SLC16A5	ENSG00000170190	8.85	0.71	12.41
MPP1	ENSG00000130830	4.66	0.38	12.36
TMEM98	ENSG00000006042	10.66	0.88	12.05
SOBP	ENSG00000112320	8.95	0.76	11.82
FLI1	ENSG00000151702	7.76	0.67	11.56
CTSH	ENSG00000103811	9.25	0.80	11.53
SEMA4D	ENSG00000187764	10.76	0.95	11.27
ADRBK2	ENSG00000100077	7.51	0.69	10.87
PLCG2	ENSG00000197943	7.87	0.73	10.79
CARD6	ENSG00000132357	7.37	0.71	10.35
IL1R1	ENSG00000115594	8.75	0.85	10.35
LONRF2	ENSG00000170500	7.66	0.78	9.83
STK33	ENSG00000130413	6.70	0.70	9.50
MFNG	ENSG00000100060	7.74	0.82	9.50
ARRDC4	ENSG00000140450	7.42	0.78	9.49
COL6A1	ENSG00000142156	5.83	0.62	9.39
EVI2A	ENSG00000126860	8.64	0.93	9.31
ARHGEF3	ENSG00000163947	8.32	0.90	9.25
CREG1	ENSG00000143162	5.70	0.62	9.24
FES	ENSG00000182511	8.93	0.98	9.13
XAF1	ENSG00000132530	7.91	0.87	9.12
SMU1	ENSG00000122692	1.22	0.14	9.05
KIAA1462	ENSG00000165757	5.60	0.63	8.92
GALM	ENSG00000143891	4.88	0.55	8.85
SLC41A2	ENSG00000136052	5.52	0.63	8.76
CD33	ENSG00000105383	6.97	0.80	8.67
HCP5	ENSG00000206337	4.66	0.54	8.62
CDO1	ENSG00000129596	8.92	1.04	8.61
ST3GAL6	ENSG00000064225	6.21	0.74	8.42
PROM2	ENSG00000155066	3.51	0.42	8.41
HLA-F	ENSG00000204642	4.66	0.56	8.33
VSTM4	ENSG00000165633	9.52	1.14	8.32

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

FAM120AOS	ENSG00000188938	1.96	0.24	8.22
MAPRE3	ENSG00000084764	3.13	0.39	8.02
WWC1	ENSG00000113645	7.69	0.96	8.01
LYN	ENSG00000254087	4.39	0.55	7.95
FAM107A	ENSG00000168309	10.63	1.35	7.86
NLRP3	ENSG00000162711	7.77	1.00	7.73
ZNF630	ENSG00000221994	4.04	0.52	7.73
UBE2R2	ENSG00000107341	1.32	0.17	7.70
TP53I11	ENSG00000175274	7.11	0.92	7.70
ZMAT1	ENSG00000166432	7.78	1.01	7.69
RHOD	ENSG00000173156	3.14	0.41	7.69
FAM84B	ENSG00000168672	6.42	0.84	7.64
ACSF2	ENSG00000167107	6.25	0.83	7.57
OAS2	ENSG00000111335	7.31	0.97	7.55
FMNL3	ENSG00000161791	4.76	0.63	7.53
PHF2	ENSG00000197724	1.70	0.23	7.51
CCDC113	ENSG00000103021	3.90	0.52	7.49
RAB20	ENSG00000139832	5.48	0.74	7.42
CIITA	ENSG00000179583	11.16	1.51	7.38
OLFML1	ENSG00000183801	11.18	1.52	7.37
ZNF681	ENSG00000196172	3.06	0.42	7.32
IL17RD	ENSG00000144730	6.91	0.95	7.32
IL15RA	ENSG00000134470	4.08	0.56	7.25
COLEC12	ENSG00000158270	12.56	1.74	7.22
NUDT7	ENSG00000140876	5.18	0.72	7.22
FAM78A	ENSG00000126882	6.75	0.95	7.13
TEK	ENSG00000120156	6.06	0.86	7.09
GAB3	ENSG00000160219	8.30	1.18	7.05
LRRC8B	ENSG00000197147	4.38	0.62	7.03
OAS1	ENSG00000089127	9.13	1.30	7.03
PLXNC1	ENSG00000136040	10.16	1.45	7.03
DDIT4	ENSG00000168209	7.48	1.08	6.94
RRAGD	ENSG00000025039	5.69	0.83	6.89
RAVER2	ENSG00000162437	5.26	0.76	6.88
ZNF439	ENSG00000171291	3.14	0.46	6.87
TSPYL5	ENSG00000180543	5.63	0.83	6.81
FAM149A	ENSG00000109794	6.23	0.91	6.81
GCA	ENSG00000115271	7.84	1.18	6.66
SLC43A3	ENSG00000134802	6.03	0.91	6.65
FAM49A	ENSG00000197872	6.18	0.94	6.61
CSF1R	ENSG00000182578	10.46	1.58	6.61
RP11-872D17.8	ENSG00000254979	5.81	0.88	6.59
ZNF677	ENSG00000197928	3.67	0.56	6.54
NDN	ENSG00000182636	11.41	1.75	6.52
PGM5	ENSG00000154330	10.65	1.64	6.50

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

HLA-DMB	ENSG00000242574	9.64	1.48	6.50
CD68	ENSG00000129226	4.91	0.76	6.46
LDB2	ENSG00000169744	9.87	1.53	6.43
FZD3	ENSG00000104290	4.28	0.67	6.40
NAP1L3	ENSG00000186310	5.07	0.79	6.40
EIF4E3	ENSG00000163412	5.53	0.87	6.38
MTSS1	ENSG00000170873	10.62	1.67	6.37
NYNRIN	ENSG00000205978	8.91	1.40	6.37
NFATC2	ENSG00000101096	6.13	0.96	6.37
STRBP	ENSG00000165209	2.00	0.31	6.35
FMO4	ENSG00000076258	6.31	1.00	6.34
HERC6	ENSG00000138642	5.07	0.80	6.34
MX1	ENSG00000157601	6.94	1.10	6.33
RTP4	ENSG00000136514	4.76	0.75	6.32
ZNF516	ENSG00000101493	8.98	1.42	6.32
AC099522.1	ENSG00000183900	3.21	0.51	6.31
NCKAP1L	ENSG00000123338	10.93	1.74	6.30
LNX1	ENSG00000072201	6.06	0.96	6.29
CTD-3184A7.4	ENSG00000232442	3.10	0.49	6.28
FAM213A	ENSG00000122378	11.50	1.83	6.28
HSPA12A	ENSG00000165868	7.56	1.21	6.25
KCNC3	ENSG00000131398	11.08	1.79	6.20
MAGEH1	ENSG00000187601	3.71	0.60	6.20
HOMER2	ENSG00000103942	6.10	0.98	6.20
RP11-18F14.2	ENSG00000261128	5.12	0.83	6.18
CLEC2B	ENSG00000110852	5.65	0.92	6.17
TSPAN33	ENSG00000158457	4.57	0.74	6.16
DNAJB2	ENSG00000135924	1.63	0.27	6.14
NUP210	ENSG00000132182	5.25	0.86	6.12
SLC18B1	ENSG00000146409	3.87	0.63	6.11
FOXD2	ENSG00000186564	8.63	1.42	6.09
FKBP5	ENSG00000096060	9.12	1.50	6.08
CLEC2D	ENSG00000069493	4.49	0.74	6.06
CPNE8	ENSG00000139117	7.24	1.20	6.05
SLC12A7	ENSG00000113504	8.46	1.40	6.04
PALD1	ENSG00000107719	5.66	0.95	5.98
MSRB2	ENSG00000148450	2.29	0.38	5.97
HIVEP3	ENSG00000127124	7.08	1.19	5.96
F8	ENSG00000185010	4.02	0.68	5.95
FOXD1	ENSG00000251493	3.07	0.52	5.95
ENOSF1	ENSG00000132199	2.79	0.47	5.93
ZNF43	ENSG00000198521	2.38	0.40	5.93
CORO1A	ENSG00000102879	7.28	1.23	5.93
TNS1	ENSG00000079308	5.61	0.95	5.90
SLC29A3	ENSG00000198246	3.61	0.61	5.90

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

CTD-2368P22.1	ENSG00000176593	3.90	0.66	5.89
CLEC1A	ENSG00000150048	12.57	2.14	5.88
MFAP3L	ENSG00000198948	4.19	0.71	5.88
SRGAP3	ENSG00000196220	8.29	1.41	5.87
AC009469.1	ENSG00000256309	6.95	1.19	5.86
ZNF169	ENSG00000175787	2.90	0.49	5.86
HLA-DQB1	ENSG00000179344	12.27	2.09	5.86
FOXD2-AS1	ENSG00000237424	6.36	1.09	5.86
GTPBP6	ENSG00000178605	1.63	0.28	5.85
AC099522.2	ENSG00000255883	1.74	0.30	5.84
STARD8	ENSG00000130052	4.29	0.73	5.84
C7orf31	ENSG00000153790	5.81	0.99	5.84
TMEM150C	ENSG00000249242	5.92	1.02	5.82
HLA-DMA	ENSG00000204257	6.21	1.07	5.81
ZNF135	ENSG00000176293	8.21	1.42	5.79
SURF6	ENSG00000148296	1.40	0.24	5.76
CACHD1	ENSG00000158966	4.10	0.71	5.75
TNFRSF1B	ENSG00000028137	11.62	2.02	5.75
CXCR4	ENSG00000121966	10.71	1.87	5.73
PYGL	ENSG00000100504	3.66	0.64	5.72
ZNF606	ENSG00000166704	2.68	0.47	5.71
SPATA5L1	ENSG00000171763	1.64	0.29	5.70
ZFP3	ENSG00000180787	3.50	0.62	5.66
ZNF354C	ENSG00000177932	4.99	0.89	5.61
SPRY1	ENSG00000164056	6.38	1.14	5.59
P2RX7	ENSG00000089041	5.21	0.93	5.58
CXADR	ENSG00000154639	9.27	1.66	5.58
FAM105A	ENSG00000145569	8.54	1.53	5.56
HLA-C	ENSG00000204525	1.83	0.33	5.55
SCRN2	ENSG00000141295	2.07	0.37	5.55
B3GALNT1	ENSG00000169255	2.99	0.54	5.55
ZNF334	ENSG00000198185	8.03	1.45	5.54
ST6GALNAC6	ENSG00000160408	1.73	0.31	5.53
MAP3K5	ENSG00000197442	4.39	0.79	5.53
GIMAP2	ENSG00000106560	6.21	1.12	5.52
TMCC3	ENSG00000057704	8.96	1.63	5.51
GPR27	ENSG00000170837	8.75	1.59	5.50
GKAP1	ENSG00000165113	2.56	0.46	5.50
MANBA	ENSG00000109323	1.40	0.25	5.49
IGFLR1	ENSG00000126246	3.37	0.62	5.47
ITGB2	ENSG00000160255	7.02	1.29	5.45
SLC25A30	ENSG00000174032	1.78	0.33	5.45
TSPAN18	ENSG00000157570	10.87	1.99	5.45
LINC00654	ENSG00000205181	7.56	1.39	5.45
LURAP1	ENSG00000171357	3.48	0.64	5.44

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RTN1	ENSG00000139970	6.15	1.13	5.43
CEP44	ENSG00000164118	1.36	0.25	5.43
SERPINA1	ENSG00000197249	8.05	1.48	5.42
HLA-DQA1	ENSG00000196735	12.51	2.31	5.42
CARD16	ENSG00000204397	6.44	1.19	5.41
PARD6G	ENSG00000178184	7.14	1.32	5.40
CD163	ENSG00000177575	13.11	2.44	5.38
ARHGDIB	ENSG00000111348	8.07	1.51	5.36
ARMCX2	ENSG00000184867	4.92	0.92	5.35
CCDC69	ENSG00000198624	5.32	0.99	5.35
LINC00526	ENSG00000264575	2.32	0.43	5.34
MTUS1	ENSG00000129422	8.68	1.63	5.32
ITIH5	ENSG00000123243	10.45	1.97	5.30
TMEM107	ENSG00000179029	1.88	0.36	5.29
CD93	ENSG00000125810	13.02	2.47	5.27
IRF5	ENSG00000128604	5.79	1.10	5.27
PPIL3	ENSG00000240344	1.42	0.27	5.25
GMPR	ENSG00000137198	5.30	1.01	5.25
SLC43A1	ENSG00000149150	2.95	0.56	5.24
SCAND2P	ENSG00000176700	1.90	0.36	5.24
HLA-B	ENSG00000234745	2.41	0.46	5.23
C14orf132	ENSG00000227051	6.49	1.24	5.22
STAB1	ENSG00000010327	11.53	2.21	5.21
ADORA3	ENSG00000121933	11.01	2.11	5.21
IFIH1	ENSG00000115267	2.80	0.54	5.21
RNF130	ENSG00000113269	2.17	0.42	5.20
FAM69B	ENSG00000165716	5.69	1.09	5.20
VANGL2	ENSG00000162738	8.75	1.69	5.19
AKAP17A	ENSG00000197976	2.43	0.47	5.18
AIF1	ENSG00000204472	11.38	2.20	5.18
HLA-DPA1	ENSG00000231389	10.63	2.05	5.18
ZNF138	ENSG00000197008	1.52	0.29	5.18
CTSZ	ENSG00000101160	1.88	0.36	5.17
HLA-DMB	ENSG00000248993	7.88	1.53	5.16
SARDH	ENSG00000123453	5.84	1.13	5.15
ROBO4	ENSG00000154133	6.68	1.30	5.15
LY6E	ENSG00000160932	2.85	0.55	5.15
THEMIS2	ENSG00000130775	6.87	1.34	5.14
VWA1	ENSG00000179403	5.14	1.00	5.12
GTDC2	ENSG00000144647	1.80	0.35	5.11
TXNIP	ENSG00000117289	4.55	0.89	5.10
MYO1D	ENSG00000176658	8.23	1.61	5.10
LAIR1	ENSG00000167613	12.32	2.42	5.10
SIMC1	ENSG00000170085	2.08	0.41	5.08
WAS	ENSG00000015285	7.90	1.56	5.07

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C2CD2	ENSG00000157617	1.90	0.38	5.05
AGPAT4	ENSG00000026652	2.61	0.52	5.05
PLCXD1	ENSG00000182378	2.66	0.53	5.05
EPHB3	ENSG00000182580	6.00	1.19	5.04
MPZL2	ENSG00000149573	11.03	2.19	5.04
VSIG4	ENSG00000155659	12.34	2.45	5.04
SPNS2	ENSG00000183018	5.27	1.05	5.04
EPB41L3	ENSG00000082397	10.28	2.04	5.04
DCHS1	ENSG00000166341	9.02	1.79	5.04
RP11-708J19.1	ENSG00000260236	3.08	0.61	5.03
BST2	ENSG00000130303	8.42	1.67	5.03
SULT1A2	ENSG00000197165	7.95	1.58	5.03
LIFR-AS1	ENSG00000244968	4.03	0.80	5.03
EPHA4	ENSG00000116106	3.66	0.73	5.03
PPP1R3B	ENSG00000173281	3.58	0.71	5.02
EAF2	ENSG00000145088	3.28	0.65	5.02
ABLIM3	ENSG00000173210	2.61	0.52	5.00
AGBL3	ENSG00000146856	3.24	0.65	5.00
ZNF691	ENSG00000164011	2.22	0.45	4.99
ASMTL-AS1	ENSG00000236017	2.89	0.58	4.99
TENM4	ENSG00000149256	9.83	1.97	4.98
IFI30	ENSG00000216490	4.99	1.00	4.97
RAPGEF4	ENSG00000091428	7.74	1.56	4.95
AC006160.8	ENSG00000254360	3.08	0.62	4.95
KIAA0040	ENSG00000235750	7.63	1.54	4.94
POC1B	ENSG00000139323	1.41	0.29	4.94
NET1	ENSG00000173848	5.23	1.06	4.94
PDZD2	ENSG00000133401	5.13	1.04	4.94
AL356740.1	ENSG00000234603	2.38	0.48	4.93
SYTL3	ENSG00000164674	2.97	0.60	4.93
HSD17B14	ENSG00000087076	6.09	1.24	4.93
KIAA0040	ENSG00000265365	7.59	1.54	4.92
PRKAR2B	ENSG00000005249	4.79	0.97	4.92
ASRGL1	ENSG00000162174	3.73	0.76	4.91
TSPAN14	ENSG00000108219	1.73	0.35	4.91
SFMBT2	ENSG00000198879	9.29	1.89	4.91
HLA-DOA	ENSG00000204252	9.54	1.94	4.91
C9orf16	ENSG00000171159	1.99	0.41	4.90
KHDRBS3	ENSG00000131773	5.67	1.16	4.90
APOBEC3G	ENSG00000239713	3.39	0.69	4.90
C9orf72	ENSG00000147894	2.45	0.50	4.90
CORO2B	ENSG00000103647	5.44	1.11	4.89
TBXAS1	ENSG00000059377	5.74	1.17	4.89
CD74	ENSG00000019582	11.40	2.33	4.89
GNG2	ENSG00000186469	7.54	1.54	4.88

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

GOLGA2	ENSG00000167110	1.01	0.21	4.88
LYSMD2	ENSG00000140280	1.90	0.39	4.88
MITD1	ENSG00000158411	1.57	0.32	4.88
CTSS	ENSG00000163131	8.87	1.82	4.87
NSMCE4A	ENSG00000107672	1.09	0.22	4.87
SORL1	ENSG00000137642	10.34	2.13	4.86
RASSF4	ENSG00000107551	5.92	1.22	4.86
CPXM1	ENSG00000088882	11.81	2.43	4.86
FAM174B	ENSG00000185442	5.04	1.04	4.85
H1FX-AS1	ENSG00000206417	3.97	0.82	4.85
SERPING1	ENSG00000149131	10.74	2.22	4.84
ARHGAP30	ENSG00000186517	9.91	2.05	4.83
TOPORS-AS1	ENSG00000235453	2.06	0.43	4.82
NRP1	ENSG00000099250	3.83	0.79	4.82
GALT	ENSG00000213930	2.49	0.52	4.82
PTPRE	ENSG00000132334	5.95	1.24	4.81
RAPGEF3	ENSG00000079337	5.41	1.13	4.81
TLR2	ENSG00000137462	11.92	2.49	4.80
ERO1LB	ENSG00000086619	1.91	0.40	4.80
FAM117A	ENSG00000121104	2.80	0.58	4.79
LCP2	ENSG00000043462	10.56	2.21	4.79
CSF3R	ENSG00000119535	11.15	2.33	4.78
SH3TC1	ENSG00000125089	11.35	2.37	4.78
MS4A6A	ENSG00000110077	11.59	2.43	4.77
MXRA5	ENSG00000101825	9.51	1.99	4.77
SLA	ENSG00000155926	10.36	2.17	4.77
TSR2	ENSG00000158526	1.14	0.24	4.77
DDX58	ENSG00000107201	1.92	0.40	4.77
FAAH	ENSG00000117480	5.39	1.13	4.76
CD4	ENSG00000010610	11.66	2.45	4.76
C7orf63	ENSG00000105792	4.23	0.89	4.76
MGAT4A	ENSG00000071073	9.03	1.90	4.75
RTN4RL1	ENSG00000185924	7.50	1.58	4.75
NTN1	ENSG00000065320	9.69	2.05	4.73
TIGD7	ENSG00000140993	2.12	0.45	4.73
CXCL12	ENSG00000107562	4.28	0.91	4.73
RPS6KA1	ENSG00000117676	3.17	0.67	4.73
ECHDC2	ENSG00000121310	2.78	0.59	4.72
FAM198A	ENSG00000144649	11.01	2.33	4.72
SERPINF1	ENSG00000132386	11.61	2.46	4.72
COPG2	ENSG00000158623	1.29	0.27	4.71
FCGR3A	ENSG00000203747	11.24	2.39	4.71
ZNF680	ENSG00000173041	2.24	0.48	4.71
GREB1	ENSG00000196208	8.39	1.78	4.71
ANGPTL2	ENSG00000136859	5.17	1.10	4.70

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PLXDC1	ENSG00000161381	9.00	1.91	4.70
HTRA2	ENSG00000115317	1.40	0.30	4.70
C1QA	ENSG00000173372	12.22	2.60	4.70
HESX1	ENSG00000163666	3.00	0.64	4.70
KCNMB3	ENSG00000171121	3.53	0.75	4.70
NTRK3	ENSG00000140538	10.68	2.28	4.69
FAM66C	ENSG00000226711	2.27	0.48	4.69
UBAP1	ENSG00000165006	1.24	0.26	4.69
AS3MT	ENSG00000214435	5.07	1.08	4.68
KLRAP1	ENSG00000256667	2.20	0.47	4.67
WASH4P	ENSG00000234769	2.64	0.57	4.67
XXbac-BPG246D15.8	ENSG00000204261	2.39	0.51	4.66
CDH1	ENSG00000039068	10.72	2.30	4.66
EPSTI1	ENSG00000133106	2.93	0.63	4.65
SLC1A3	ENSG00000079215	11.51	2.48	4.65
C8orf42	ENSG00000180190	8.28	1.78	4.64
AKNA	ENSG00000106948	4.04	0.87	4.64
ANXA3	ENSG00000138772	4.57	0.98	4.64
CREBZF	ENSG00000137504	1.63	0.35	4.63
MDH1B	ENSG00000138400	3.97	0.86	4.63
SPEF2	ENSG00000152582	4.27	0.92	4.63
AEBP1	ENSG00000106624	4.95	1.07	4.63
OLFML2B	ENSG00000162745	5.64	1.22	4.63
HLA-DRA	ENSG00000204287	11.07	2.40	4.62
DOCK2	ENSG00000134516	3.43	0.74	4.62
A2M	ENSG00000175899	10.64	2.31	4.61
C1QC	ENSG00000159189	11.24	2.44	4.61
AARS2	ENSG00000124608	1.45	0.31	4.60
INPP5D	ENSG00000168918	8.00	1.74	4.60
PSMB9	ENSG00000240065	2.49	0.54	4.60
FUNDC2	ENSG00000165775	1.28	0.28	4.59
ZNF626	ENSG00000188171	2.02	0.44	4.59
APIP	ENSG00000149089	1.37	0.30	4.59
C1QB	ENSG00000173369	11.96	2.61	4.59
FAHD2A	ENSG00000115042	1.00	0.22	4.58
ENOX1	ENSG00000120658	4.15	0.91	4.57
HDHD2	ENSG00000167220	1.48	0.33	4.56
NLRP1	ENSG00000091592	2.08	0.46	4.56
AKR1C3	ENSG00000196139	5.39	1.18	4.55
SORBS1	ENSG00000095637	6.97	1.53	4.55
DMKN	ENSG00000161249	8.94	1.97	4.55
FGD2	ENSG00000146192	9.91	2.18	4.55
USP18	ENSG00000184979	2.40	0.53	4.55
LAPTM5	ENSG00000162511	10.71	2.36	4.54
DAPK2	ENSG00000035664	6.19	1.36	4.54

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ZNRD1-AS1	ENSG00000204623	2.43	0.54	4.53
COX18	ENSG00000163626	1.14	0.25	4.53
RNASEH2C	ENSG00000172922	1.60	0.35	4.53
ADAM23	ENSG00000114948	5.45	1.21	4.51
CDH23	ENSG00000107736	11.29	2.51	4.49
USP51	ENSG00000247746	4.04	0.90	4.48
N6AMT2	ENSG00000150456	1.21	0.27	4.48
FAM162A	ENSG00000114023	1.41	0.32	4.48
HCLS1	ENSG00000180353	10.13	2.26	4.47
OLFM2	ENSG00000105088	6.60	1.48	4.47
C3	ENSG00000125730	10.92	2.45	4.47
SHANK3	ENSG00000251322	5.08	1.14	4.47
ZNF204P	ENSG00000204789	7.01	1.57	4.46
CLYBL	ENSG00000125246	3.14	0.70	4.46
CCDC74A	ENSG00000163040	4.91	1.10	4.45
ZNF671	ENSG00000083814	2.31	0.52	4.45
USF2	ENSG00000105698	1.66	0.37	4.45
LRFN1	ENSG00000128011	4.26	0.96	4.45
ADAM28	ENSG00000042980	9.34	2.10	4.44
RNASET2	ENSG00000026297	4.76	1.07	4.44
RAB9B	ENSG00000123570	3.34	0.75	4.44
CCDC8	ENSG00000169515	9.31	2.10	4.44
FCGBP	ENSG00000090920	11.53	2.61	4.43
KLHL3	ENSG00000146021	7.93	1.79	4.43
ATP8A1	ENSG00000124406	6.13	1.38	4.43
SLC37A2	ENSG00000134955	5.89	1.33	4.43
GM2A	ENSG00000196743	1.40	0.32	4.42
RP11-727A23.5	ENSG00000247137	3.15	0.71	4.42
BHMT2	ENSG00000132840	5.38	1.22	4.42
HLA-DRB5	ENSG00000198502	11.06	2.51	4.41
SLC15A2	ENSG00000163406	7.52	1.71	4.40
RAD9A	ENSG00000172613	1.71	0.39	4.40
OAF	ENSG00000184232	5.36	1.22	4.40
TOP1	ENSG00000198900	1.50	0.34	4.39
GPR160	ENSG00000173890	2.63	0.60	4.38
SEC24B-AS1	ENSG00000247950	2.60	0.59	4.38
CHST10	ENSG00000115526	1.45	0.33	4.38
ICAM1	ENSG00000090339	5.37	1.23	4.37
CLEC11A	ENSG00000105472	6.33	1.45	4.37
LRPAP1	ENSG00000163956	1.06	0.24	4.37
MIR600HG	ENSG00000236901	4.42	1.01	4.37
NAPB	ENSG00000125814	1.68	0.38	4.36
LIFR	ENSG00000113594	3.32	0.76	4.36
PHF7	ENSG00000010318	1.25	0.29	4.36
HLA-DPB1	ENSG00000223865	10.89	2.50	4.35

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MS4A7	ENSG00000166927	9.91	2.28	4.35
SLC25A35	ENSG00000125434	2.02	0.47	4.35
SLC25A6	ENSG00000169100	1.63	0.38	4.35
RP11-213G2.3	ENSG00000165121	2.23	0.51	4.34
CIZ1	ENSG00000148337	1.18	0.27	4.34
RP11-383H13.1	ENSG00000235531	4.41	1.02	4.34
POLN	ENSG00000130997	1.78	0.41	4.33
THBS4	ENSG00000113296	4.34	1.00	4.32
RP11-315D16.2	ENSG00000260007	4.38	1.01	4.32
ACSS3	ENSG00000111058	7.51	1.74	4.32
FRS3	ENSG00000137218	1.91	0.44	4.32
TMEM220	ENSG00000187824	5.18	1.20	4.32
BHLHE41	ENSG00000123095	5.56	1.29	4.32
ADPGK	ENSG00000159322	1.03	0.24	4.31
OARD1	ENSG00000124596	1.47	0.34	4.31
SRSF12	ENSG00000154548	5.49	1.27	4.30
TMEM100	ENSG00000166292	11.71	2.72	4.30
CCNO	ENSG00000152669	2.34	0.54	4.30
NXNL2	ENSG00000130045	4.17	0.97	4.29
MBNL3	ENSG00000076770	9.25	2.16	4.29
CEBPA	ENSG00000245848	5.34	1.25	4.29
ANKRD23	ENSG00000163126	1.20	0.28	4.28
AC008738.1	ENSG00000230259	5.31	1.24	4.28
SLC7A8	ENSG00000092068	9.95	2.33	4.28
ESAM	ENSG00000149564	6.50	1.52	4.28
MCTP1	ENSG00000175471	3.88	0.91	4.27
LSR	ENSG00000105699	5.28	1.24	4.27
TM6SF1	ENSG00000136404	8.95	2.10	4.26
METTL7A	ENSG00000185432	7.89	1.85	4.26
CYP27A1	ENSG00000135929	10.02	2.35	4.26
CDH5	ENSG00000179776	9.85	2.31	4.26
SIGLEC10	ENSG00000142512	9.66	2.27	4.25
WNK4	ENSG00000126562	8.64	2.04	4.25
PPWD1	ENSG00000113593	1.06	0.25	4.24
IRF2	ENSG00000168310	1.45	0.34	4.24
DCAF12	ENSG00000198876	1.39	0.33	4.24
EPB41L4A	ENSG00000129595	7.84	1.85	4.23
TNFSF12	ENSG00000239697	2.53	0.60	4.23
GATM	ENSG00000171766	8.00	1.89	4.23
GSDMD	ENSG00000104518	1.77	0.42	4.23
HLA-DRB1	ENSG00000196126	11.27	2.67	4.23
RASSF2	ENSG00000101265	10.80	2.56	4.23
ATG16L2	ENSG00000168010	2.69	0.64	4.22
CCDC66	ENSG00000180376	1.43	0.34	4.22
C9orf37	ENSG00000203993	1.79	0.42	4.22

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ENG	ENSG00000106991	2.49	0.59	4.22
FBXO4	ENSG00000151876	1.28	0.30	4.22
C19orf66	ENSG00000130813	2.15	0.51	4.21
PREX1	ENSG00000124126	4.87	1.16	4.21
CDADC1	ENSG00000102543	1.34	0.32	4.21
OSBPL3	ENSG00000070882	2.71	0.64	4.20
RGS1	ENSG00000090104	10.56	2.51	4.20
RP11-231E4.4	ENSG00000264247	1.75	0.42	4.20
C2orf40	ENSG00000119147	11.30	2.69	4.20
ACOX2	ENSG00000168306	2.04	0.49	4.19
B3GNT1	ENSG00000174684	1.97	0.47	4.19
POU2F2	ENSG00000028277	5.70	1.36	4.19
VASH1	ENSG00000071246	3.58	0.85	4.19
NTRK2	ENSG00000148053	9.33	2.23	4.19
SREBF1	ENSG00000072310	2.41	0.58	4.19
CYP4V2	ENSG00000145476	2.89	0.69	4.19
FBXO6	ENSG00000116663	2.35	0.56	4.19
ARHGEF6	ENSG00000129675	2.93	0.70	4.18
AGXT2L2	ENSG00000175309	1.87	0.45	4.17
PLEKHG1	ENSG00000120278	6.39	1.53	4.17
AFAP1L2	ENSG00000169129	6.11	1.47	4.16
NEB	ENSG00000183091	7.04	1.69	4.16
ABCC9	ENSG00000069431	10.00	2.40	4.16
RP11-333E1.1	ENSG00000261879	3.39	0.82	4.16
DICER1-AS1	ENSG00000235706	4.10	0.99	4.16
ITGAX	ENSG00000140678	9.91	2.39	4.15
EYA1	ENSG00000104313	9.97	2.41	4.15
ITGAM	ENSG00000169896	9.03	2.18	4.14
ZNF767	ENSG00000133624	2.55	0.62	4.14
CCND2	ENSG00000118971	9.64	2.33	4.14
SPARCL1	ENSG00000152583	10.19	2.46	4.14
FBXL14	ENSG00000171823	2.05	0.50	4.14
TTYH2	ENSG00000141540	5.96	1.44	4.13
CARD8	ENSG00000105483	1.93	0.47	4.12
RP11-488C13.7	ENSG00000258610	4.17	1.01	4.12
FAM221A	ENSG00000188732	5.63	1.37	4.12
ITM2A	ENSG00000078596	9.97	2.42	4.12
PRMT10	ENSG00000164169	1.38	0.34	4.12
RP11-856B14.1	ENSG00000260233	3.43	0.83	4.11
CPXM2	ENSG00000121898	11.13	2.71	4.11
CACNA2D2	ENSG00000007402	8.89	2.16	4.11
APTX	ENSG00000137074	1.26	0.31	4.11
TSSK6	ENSG00000178093	2.04	0.50	4.11
THUMPD2	ENSG00000138050	1.08	0.26	4.11
TYROBP	ENSG00000011600	11.31	2.75	4.11

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F13A1	ENSG00000124491	10.36	2.52	4.11
CDAN1	ENSG00000140326	1.30	0.32	4.10
PTGES2	ENSG00000148334	1.12	0.27	4.10
AL133458.1	ENSG00000197146	6.64	1.62	4.09
NT5M	ENSG00000205309	2.98	0.73	4.09
CTB-131B5.4	ENSG00000245146	1.96	0.48	4.09
APOBR	ENSG00000184730	7.11	1.74	4.09
RP11-705C15.2	ENSG00000256594	2.30	0.56	4.09
CD34	ENSG00000174059	6.30	1.54	4.09
SOX13	ENSG00000143842	3.29	0.81	4.08
HEBP1	ENSG00000013583	1.15	0.28	4.08
NUDT6	ENSG00000170917	1.53	0.38	4.08
ZNF540	ENSG00000171817	5.16	1.27	4.08
ENPP2	ENSG00000136960	4.77	1.17	4.07
RP11-203J24.9	ENSG00000257524	2.02	0.50	4.07
GIMAP5	ENSG00000196329	7.66	1.88	4.07
RP11-514O12.4	ENSG00000249141	3.98	0.98	4.07
C1orf162	ENSG00000143110	6.77	1.67	4.06
SEPT4	ENSG00000108387	5.66	1.40	4.05
ITFG2	ENSG00000111203	1.35	0.33	4.05
BEND7	ENSG00000165626	2.67	0.66	4.05
ACAP1	ENSG00000072818	4.66	1.15	4.05
TMEM68	ENSG00000167904	1.43	0.35	4.05
AQP1	ENSG00000240583	10.01	2.47	4.05
KIAA1467	ENSG00000084444	2.14	0.53	4.05
RP11-325D5.3	ENSG00000248421	1.34	0.33	4.04
SASH3	ENSG00000122122	8.54	2.12	4.04
KCNJ2	ENSG00000123700	5.61	1.39	4.03
AC132217.4	ENSG00000240801	11.11	2.75	4.03
ABAT	ENSG00000183044	4.35	1.08	4.03
PDE6A	ENSG00000132915	6.69	1.66	4.03
ACSL5	ENSG00000197142	6.39	1.59	4.02
PDE7A	ENSG00000205268	2.09	0.52	4.02
LETMD1	ENSG00000050426	1.77	0.44	4.01
TIE1	ENSG00000066056	6.02	1.50	4.01
SLC11A2	ENSG00000110911	1.26	0.31	4.01
ZNF594	ENSG00000180626	2.71	0.68	4.00
NFATC4	ENSG00000100968	3.48	0.87	4.00
ADAMTSL4	ENSG00000143382	5.34	1.33	4.00
TMEM56	ENSG00000152078	2.81	0.70	4.00
HMHA1	ENSG00000180448	8.12	2.03	4.00
DPP7	ENSG00000176978	1.83	0.46	3.99
RNPC3	ENSG00000185946	2.72	0.68	3.99
ENGASE	ENSG00000167280	2.42	0.61	3.99
ZNF595	ENSG00000197701	1.51	0.38	3.98

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MPEG1	ENSG00000197629	10.66	2.68	3.98
LCP1	ENSG00000136167	9.66	2.43	3.98
FRAS1	ENSG00000138759	8.33	2.10	3.97
RILPL2	ENSG00000150977	1.75	0.44	3.97
TRIM68	ENSG00000167333	1.17	0.29	3.97
SNTA1	ENSG00000101400	2.34	0.59	3.97
MYO1F	ENSG00000142347	6.95	1.75	3.97
NPL	ENSG00000135838	4.10	1.03	3.97
ZSCAN18	ENSG00000121413	4.66	1.17	3.97
LAMB3	ENSG00000196878	2.63	0.66	3.97
GUCY1B3	ENSG00000061918	3.50	0.88	3.96
CCDC88C	ENSG00000015133	3.47	0.88	3.96
SDCBP2	ENSG00000125775	2.60	0.66	3.95
RFX1	ENSG00000132005	1.79	0.45	3.95
RP11-323F5.2	ENSG00000247708	1.53	0.39	3.95
PIK3AP1	ENSG00000155629	7.75	1.96	3.94
H19	ENSG00000130600	10.57	2.68	3.94
TNFSF12-TNFSF13	ENSG00000248871	3.19	0.81	3.94
ZNF675	ENSG00000197372	1.41	0.36	3.94
ATL2	ENSG00000119787	2.32	0.59	3.94
SLC7A2	ENSG00000003989	7.38	1.88	3.94
SEMA4C	ENSG00000168758	1.94	0.49	3.93
COL5A3	ENSG00000080573	4.21	1.07	3.93
CYB561	ENSG00000008283	2.60	0.66	3.93
CYBA	ENSG00000051523	7.65	1.95	3.93
ZNF572	ENSG00000180938	3.34	0.85	3.92
CASP1	ENSG00000137752	3.99	1.02	3.91
PTPRC	ENSG00000081237	7.53	1.92	3.91
KLF9	ENSG00000119138	5.70	1.46	3.91
TMEM132C	ENSG00000181234	10.02	2.56	3.91
AMY2B	ENSG00000240038	4.16	1.07	3.91
EFNB1	ENSG00000090776	3.88	0.99	3.90
RARRES2	ENSG00000106538	10.64	2.72	3.90
OGN	ENSG00000106809	10.56	2.71	3.90
NSUN5P1	ENSG00000223705	2.29	0.59	3.90
CD72	ENSG00000137101	4.27	1.09	3.90
ADRBK1	ENSG00000173020	1.64	0.42	3.89
C1orf213	ENSG00000249087	2.93	0.75	3.89
SEPT1	ENSG00000180096	2.35	0.60	3.89
MPP2	ENSG00000108852	1.62	0.42	3.89
HLA-E	ENSG00000204592	1.83	0.47	3.89
CLUHP3	ENSG00000131797	2.43	0.63	3.88
RUSC1-AS1	ENSG00000225855	2.98	0.77	3.88
FREM1	ENSG00000164946	9.15	2.36	3.88
Z95704.2	ENSG00000255436	1.60	0.41	3.88

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SOD3	ENSG00000109610	6.76	1.74	3.88
FMOD	ENSG00000122176	10.51	2.71	3.88
TMEM140	ENSG00000146859	2.78	0.72	3.87
HSPA7	ENSG00000225217	9.07	2.34	3.87
LRRC37B	ENSG00000185158	1.23	0.32	3.87
TSPAN7	ENSG00000156298	10.32	2.66	3.87
GPR4	ENSG00000177464	8.86	2.29	3.87
RAMP2	ENSG00000131477	6.66	1.72	3.87
IGF2	ENSG00000167244	10.42	2.70	3.87
LPCAT2	ENSG00000087253	3.52	0.91	3.86
AK1	ENSG00000106992	2.05	0.53	3.86
MYO7A	ENSG00000137474	7.71	2.00	3.86
U2AF1L4	ENSG00000267120	1.92	0.50	3.86
CHST12	ENSG00000136213	1.44	0.37	3.86
ASB13	ENSG00000196372	2.09	0.54	3.86
RP11-1114A5.4	ENSG00000232611	3.21	0.83	3.85
AC017099.3	ENSG00000228486	3.06	0.79	3.85
NSUN6	ENSG00000241058	1.61	0.42	3.85
TMEM101	ENSG00000091947	1.25	0.33	3.85
ALOX5AP	ENSG00000132965	8.95	2.33	3.85
GID4	ENSG00000141034	1.25	0.33	3.85
BEX4	ENSG00000102409	6.98	1.81	3.85
UNC50	ENSG00000115446	1.02	0.27	3.85
VAT1L	ENSG00000171724	10.21	2.66	3.84
CLK2	ENSG00000176444	1.59	0.41	3.84
ITIH2	ENSG00000151655	10.95	2.85	3.84
PLXDC2	ENSG00000120594	10.00	2.61	3.84
ZNF253	ENSG00000256771	2.06	0.54	3.84
POPDC2	ENSG00000121577	3.55	0.93	3.84
SMOC2	ENSG00000112562	10.29	2.69	3.83
AKR1B1	ENSG00000085662	1.27	0.33	3.83
SLC2A5	ENSG00000142583	7.10	1.86	3.83
EFEMP1	ENSG00000115380	4.29	1.12	3.83
SH3BP5	ENSG00000131370	3.47	0.91	3.83
CTD-2201E18.3	ENSG00000177738	1.92	0.50	3.82
KREMEN1	ENSG00000183762	1.62	0.42	3.82
ADAM33	ENSG00000149451	8.92	2.33	3.82
ZNF185	ENSG00000147394	4.39	1.15	3.82
C7	ENSG00000112936	9.52	2.49	3.82
C12orf65	ENSG00000130921	1.29	0.34	3.82
RCSD1	ENSG00000198771	9.83	2.58	3.81
RP11-390P2.4	ENSG00000225177	4.32	1.13	3.81
PLAC9	ENSG00000189129	5.66	1.49	3.81
PEX11A	ENSG00000166821	1.74	0.46	3.80
ZNF273	ENSG00000198039	3.09	0.81	3.80

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ZNF692	ENSG00000171163	1.71	0.45	3.80
TMEM229B	ENSG00000198133	3.93	1.03	3.80
RAB24	ENSG00000169228	1.62	0.43	3.80
LAMA4	ENSG00000112769	7.76	2.04	3.80
FAM86C2P	ENSG00000160172	1.97	0.52	3.80
HDHD3	ENSG00000119431	1.61	0.42	3.80
ZSCAN12	ENSG00000158691	1.82	0.48	3.79
RP11-152N13.11	ENSG00000249376	1.43	0.38	3.79
CCDC102B	ENSG00000150636	3.01	0.79	3.79
TFEC	ENSG00000105967	5.48	1.45	3.79
IFIT1	ENSG00000185745	2.07	0.55	3.78
MYZAP	ENSG00000263155	4.47	1.18	3.78
CD14	ENSG00000170458	7.82	2.07	3.78
C10orf68	ENSG00000150076	2.02	0.53	3.78
PCSK5	ENSG00000099139	5.86	1.55	3.78
NFKBIA	ENSG00000100906	2.92	0.77	3.78
CHN1	ENSG00000128656	3.31	0.88	3.78
RP11-244O19.1	ENSG00000261534	2.50	0.66	3.78
CYTH4	ENSG00000100055	8.70	2.30	3.77
GGT5	ENSG00000099998	7.08	1.87	3.77
CTD-2528L19.6	ENSG00000267152	2.31	0.61	3.77
PECR	ENSG00000115425	1.41	0.38	3.77
SRGN	ENSG00000122862	1.41	0.38	3.76
ZRSR2	ENSG00000169249	1.56	0.41	3.76
USF1	ENSG00000158773	1.53	0.41	3.76
WHAMMP2	ENSG00000248334	2.28	0.61	3.76
AQP1	ENSG00000250424	9.43	2.51	3.76
SLIT2	ENSG00000145147	6.45	1.72	3.75
KIAA1324L	ENSG00000164659	9.13	2.43	3.75
TYMP	ENSG00000025708	8.06	2.15	3.75
WASH2P	ENSG00000146556	2.55	0.68	3.75
UQCC	ENSG00000101019	1.28	0.34	3.75
LUC7L3	ENSG00000108848	1.75	0.47	3.75
ZRSR1	ENSG00000212643	1.40	0.37	3.75
MAST4	ENSG00000069020	3.14	0.84	3.75
CFI	ENSG00000205403	11.20	2.99	3.75
TMEM79	ENSG00000163472	1.83	0.49	3.74
ZNF274	ENSG00000171606	2.26	0.60	3.74
SALL4	ENSG00000101115	6.66	1.78	3.74
ELMO1	ENSG00000155849	6.25	1.67	3.74
REEP1	ENSG00000068615	6.75	1.81	3.74
CTD-2527I21.4	ENSG00000221857	10.71	2.87	3.74
LMBR1L	ENSG00000139636	2.13	0.57	3.73
FXYD1	ENSG00000266964	10.73	2.88	3.73
SDHAF1	ENSG00000205138	1.56	0.42	3.73

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AAAS	ENSG00000094914	1.14	0.31	3.73
PCSK7	ENSG00000160613	1.02	0.27	3.73
ANKZF1	ENSG00000163516	1.61	0.43	3.73
IGIP	ENSG00000182700	2.38	0.64	3.73
CECR1	ENSG00000093072	8.74	2.35	3.73
FAM134B	ENSG00000154153	6.10	1.64	3.73
QPRT	ENSG00000103485	9.10	2.45	3.72
RNF122	ENSG00000133874	2.59	0.70	3.72
INTS6-AS1	ENSG00000236778	2.59	0.70	3.72
RP11-64P12.8	ENSG00000217576	1.60	0.43	3.71
KCNAB3	ENSG00000170049	2.23	0.60	3.71
ELMOD3	ENSG00000115459	1.49	0.40	3.71
LL0XNC01-7P3.1	ENSG00000270012	2.49	0.67	3.71
PINK1	ENSG00000158828	1.09	0.29	3.71
ADCY7	ENSG00000121281	2.71	0.73	3.70
PPARGC1B	ENSG00000155846	2.73	0.74	3.70
CLEC7A	ENSG00000172243	10.47	2.83	3.70
DAAM2	ENSG00000146122	5.20	1.41	3.69
GPSM3	ENSG00000213654	4.05	1.10	3.69
ZNF467	ENSG00000181444	7.00	1.90	3.69
FOXRED1	ENSG00000110074	1.24	0.34	3.69
INS-IGF2	ENSG00000129965	9.86	2.67	3.69
PTER	ENSG00000165983	3.21	0.87	3.69
FMO2	ENSG00000094963	9.79	2.66	3.69
GMFG	ENSG00000130755	6.52	1.77	3.69
LINC00847	ENSG00000245060	2.30	0.62	3.68
FCER1G	ENSG00000158869	7.56	2.05	3.68
CALCOCO2	ENSG00000136436	1.29	0.35	3.68
C5orf54	ENSG00000221886	2.16	0.59	3.68
FANK1	ENSG00000203780	3.06	0.83	3.67
HLA-DRB6	ENSG00000229391	10.43	2.84	3.67
SNCAIP	ENSG00000064692	5.48	1.49	3.67
RORA	ENSG00000069667	3.48	0.95	3.67
GEMIN8	ENSG00000046647	1.06	0.29	3.66
OGFR	ENSG00000060491	1.53	0.42	3.66
LYZ	ENSG00000090382	9.00	2.46	3.66
DHRS7B	ENSG00000109016	1.25	0.34	3.66
WDR52	ENSG00000206530	2.32	0.63	3.66
RP13-942N8.1	ENSG00000256092	2.36	0.64	3.66
MERTK	ENSG00000153208	3.96	1.08	3.66
NDRG2	ENSG00000165795	5.55	1.52	3.66
ZIK1	ENSG00000171649	2.05	0.56	3.66
FYB	ENSG00000082074	9.45	2.58	3.66
CCBL1	ENSG00000171097	1.48	0.40	3.66
C2orf81	ENSG00000159239	3.23	0.88	3.66

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CRABP1	ENSG00000166426	10.71	2.93	3.65
THBS2	ENSG00000186340	5.96	1.63	3.65
LST1	ENSG00000204482	7.23	1.98	3.65
HIC1	ENSG00000177374	3.24	0.89	3.65
FAM219B	ENSG00000178761	1.15	0.32	3.65
ZNF589	ENSG00000164048	1.79	0.49	3.65
GPR133	ENSG00000111452	9.41	2.58	3.64
ZNF182	ENSG00000147118	1.32	0.36	3.64
PRELP	ENSG00000188783	8.59	2.36	3.64
RP11-113K21.5	ENSG00000246067	1.40	0.39	3.63
PLEKHG4B	ENSG00000153404	8.58	2.36	3.63
CMAHP	ENSG00000168405	4.34	1.20	3.63
ANO2	ENSG00000047617	5.55	1.53	3.63
NEBL	ENSG00000078114	6.66	1.83	3.63
SAP25	ENSG00000205307	4.23	1.17	3.63
ZNF141	ENSG00000131127	2.20	0.61	3.63
RP11-145F16.2	ENSG00000261050	3.06	0.84	3.63
NCK2	ENSG00000071051	2.26	0.62	3.62
AK4	ENSG00000162433	3.43	0.95	3.62
EXTL3-AS1	ENSG00000246339	4.24	1.17	3.62
RP11-640M9.1	ENSG00000236943	1.96	0.54	3.62
NSUN5P2	ENSG00000106133	2.51	0.69	3.62
FMO1	ENSG00000010932	10.48	2.90	3.62
RP5-842K24.2	ENSG00000232160	1.78	0.49	3.61
RP11-115C21.2	ENSG00000246089	1.91	0.53	3.61
IPPK	ENSG00000127080	1.11	0.31	3.61
NIPSNAP3B	ENSG00000165028	3.36	0.93	3.61
BTN2A3P	ENSG00000124549	1.60	0.44	3.61
FRZB	ENSG00000162998	8.87	2.46	3.61
SFRP4	ENSG00000106483	10.03	2.78	3.61
CHRD	ENSG00000090539	4.48	1.24	3.61
HDAC9	ENSG00000048052	3.11	0.86	3.60
CYP4X1	ENSG00000186377	9.17	2.54	3.60
MTERFD3	ENSG00000120832	2.23	0.62	3.60
UXS1	ENSG00000115652	1.24	0.34	3.60
RP13-516M14.1	ENSG00000260563	2.85	0.79	3.60
KIAA0907	ENSG00000132680	1.49	0.42	3.60
PCBP1-AS1	ENSG00000179818	1.88	0.52	3.60
XPA	ENSG00000136936	1.11	0.31	3.60
ZNF75A	ENSG00000162086	1.15	0.32	3.60
TSPAN15	ENSG00000099282	4.21	1.17	3.60
ITGA10	ENSG00000143127	3.06	0.85	3.58
EMR2	ENSG00000127507	4.47	1.25	3.58
LINC00663	ENSG00000266904	3.75	1.05	3.58
SYPL2	ENSG00000143028	3.91	1.09	3.58

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STAG3L3	ENSG00000174353	1.74	0.49	3.58
TMCO6	ENSG00000113119	1.29	0.36	3.57
ADAM11	ENSG00000073670	3.40	0.95	3.57
TMEM106A	ENSG00000184988	1.72	0.48	3.57
DLEC1	ENSG00000008226	6.99	1.96	3.57
ACADS	ENSG00000122971	2.47	0.69	3.56
TENM3	ENSG00000218336	7.80	2.19	3.56
EXD3	ENSG00000187609	2.43	0.68	3.56
CX3CL1	ENSG00000006210	8.96	2.52	3.56
SYNPO	ENSG00000171992	2.50	0.70	3.56
CLK4	ENSG00000113240	1.89	0.53	3.55
TEX9	ENSG00000151575	1.97	0.55	3.55
TNFRSF14	ENSG00000157873	3.51	0.99	3.55
LRRC32	ENSG00000137507	4.84	1.36	3.55
RNASE1	ENSG00000129538	9.92	2.80	3.55
AC010441.1	ENSG00000269636	3.49	0.98	3.55
SMIM3	ENSG00000256235	3.49	0.98	3.55
H2AFY2	ENSG00000099284	2.50	0.71	3.55
SLC6A20	ENSG00000163817	11.05	3.12	3.55
MYH3	ENSG00000109063	2.74	0.77	3.55
CADPS2	ENSG00000081803	8.44	2.38	3.55
SPP1	ENSG00000118785	9.96	2.81	3.54
HSD17B11	ENSG00000198189	2.14	0.60	3.54
TTLL11	ENSG00000175764	1.52	0.43	3.54
PRKX	ENSG00000183943	2.26	0.64	3.54
SLC46A1	ENSG00000076351	2.27	0.64	3.54
COQ10A	ENSG00000135469	1.02	0.29	3.54
ENKD1	ENSG00000124074	2.66	0.75	3.53
MAMDC2	ENSG00000165072	6.05	1.71	3.53
PLXND1	ENSG00000004399	2.05	0.58	3.53
SFRP2	ENSG00000145423	10.26	2.91	3.53
PPM1M	ENSG00000164088	1.58	0.45	3.53
C16orf86	ENSG00000159761	4.47	1.27	3.53
CALML4	ENSG00000129007	3.19	0.90	3.53
EPHB2	ENSG00000133216	2.76	0.78	3.53
IL34	ENSG00000157368	6.32	1.79	3.52
RP11-541N10.3	ENSG00000260461	2.42	0.69	3.52
SRC	ENSG00000197122	1.56	0.44	3.52
RP11-287A8.6	ENSG00000242010	3.50	1.00	3.52
ASTN2	ENSG00000148219	4.45	1.27	3.51
ZNF737	ENSG00000237440	1.84	0.52	3.51
CLEC4A	ENSG00000111729	4.46	1.27	3.51
SLC25A38	ENSG00000144659	1.04	0.30	3.51
SAMHD1	ENSG00000101347	1.98	0.56	3.51
KDM4D	ENSG00000186280	1.88	0.54	3.51

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FAM83H	ENSG00000180921	5.65	1.61	3.51
HNMT	ENSG00000150540	9.02	2.57	3.51
FAM98C	ENSG00000130244	1.16	0.33	3.50
WDR31	ENSG00000148225	1.69	0.48	3.50
SESN1	ENSG00000080546	3.75	1.07	3.50
SCARA5	ENSG00000168079	10.51	3.00	3.50
DNASE1	ENSG00000213918	1.60	0.46	3.50
ZNF491	ENSG00000177599	1.84	0.53	3.50
CISH	ENSG00000114737	3.54	1.01	3.49
CGNL1	ENSG00000128849	4.85	1.39	3.49
C10orf32	ENSG00000166275	1.80	0.51	3.49
BDNF-AS	ENSG00000245573	3.30	0.95	3.49
C12orf76	ENSG00000174456	1.90	0.55	3.49
PRKCE	ENSG00000171132	1.04	0.30	3.48
CTSK	ENSG00000143387	4.97	1.43	3.48
DMGDH	ENSG00000132837	3.94	1.13	3.47
PARP16	ENSG00000138617	1.44	0.41	3.47
SEC31B	ENSG00000075826	1.20	0.35	3.47
FUCA1	ENSG00000179163	1.62	0.47	3.47
RP11-305E6.4	ENSG00000259994	2.33	0.67	3.47
WDR60	ENSG00000126870	1.35	0.39	3.46
TMEM129	ENSG00000168936	1.31	0.38	3.46
ZNF738	ENSG00000172687	1.37	0.39	3.46
MCF2L	ENSG00000126217	5.21	1.51	3.46
LSM5	ENSG00000106355	1.02	0.29	3.46
PAK1	ENSG00000149269	1.52	0.44	3.46
CTD-2037K23.2	ENSG00000245556	1.61	0.47	3.46
P2RX6	ENSG00000099957	3.47	1.00	3.46
ZCWPW2	ENSG00000206559	1.29	0.37	3.46
CORO7	ENSG00000262246	2.28	0.66	3.45
ZBED1	ENSG00000214717	1.14	0.33	3.45
PLEKHA6	ENSG00000143850	10.14	2.94	3.45
ATP8B4	ENSG00000104043	7.03	2.04	3.45
ZFP14	ENSG00000142065	2.52	0.73	3.44
LPIN3	ENSG00000132793	1.83	0.53	3.44
PRICKLE4	ENSG00000124593	1.15	0.33	3.44
ZNF763	ENSG00000197054	1.79	0.52	3.44
GMIP	ENSG00000089639	2.09	0.61	3.43
RP1-266L20.9	ENSG00000266896	2.14	0.63	3.43
PLCB2	ENSG00000137841	6.60	1.93	3.43
TRAF1	ENSG00000056558	5.24	1.53	3.43
RP11-572P18.1	ENSG00000220842	2.19	0.64	3.42
SLC22A17	ENSG00000092096	4.89	1.43	3.42
CORO7-PAM16	ENSG00000103426	1.78	0.52	3.42
JAK3	ENSG00000105639	6.55	1.92	3.42

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COA5	ENSG00000183513	1.53	0.45	3.42
CYP2E1	ENSG00000130649	4.33	1.27	3.42
KCNE4	ENSG00000152049	4.80	1.40	3.42
ARAP3	ENSG00000120318	4.07	1.19	3.42
WDR91	ENSG00000105875	2.10	0.61	3.41
TOMM7	ENSG00000196683	1.54	0.45	3.41
ACSL1	ENSG00000151726	1.90	0.56	3.41
C1orf204	ENSG00000188004	2.74	0.80	3.41
ZNF248	ENSG00000198105	1.20	0.35	3.41
THOC1	ENSG00000079134	1.10	0.32	3.41
ATP7B	ENSG00000123191	3.11	0.91	3.41
ZNF641	ENSG00000167528	1.91	0.56	3.40
MAP4K1	ENSG00000104814	4.43	1.30	3.40
AC135178.1	ENSG00000198150	3.22	0.95	3.40
NT5DC1	ENSG00000178425	1.49	0.44	3.39
SPAG8	ENSG00000137098	3.67	1.08	3.39
IFI44	ENSG00000137965	2.69	0.79	3.39
CYTH1	ENSG00000108669	1.61	0.48	3.39
AC004076.9	ENSG00000268163	2.36	0.70	3.39
KLKB1	ENSG00000164344	4.20	1.24	3.38
FAM110A	ENSG00000125898	1.88	0.56	3.38
PLD1	ENSG00000075651	3.58	1.06	3.38
GAL3ST4	ENSG00000197093	6.06	1.79	3.38
TCN2	ENSG00000185339	3.36	0.99	3.38
ICA1	ENSG00000003147	5.79	1.72	3.37
DNHD1	ENSG00000179532	2.69	0.80	3.37
GS1-358P8.4	ENSG00000260822	2.41	0.72	3.37
HCST	ENSG00000126264	7.08	2.10	3.37
LRP2BP	ENSG00000109771	3.23	0.96	3.37
NUPL2	ENSG00000136243	1.23	0.37	3.37
AP000346.2	ENSG00000211683	2.56	0.76	3.37
ATP6AP1L	ENSG00000205464	2.55	0.76	3.36
SFRP1	ENSG00000104332	9.18	2.73	3.36
PTPDC1	ENSG00000158079	1.93	0.57	3.36
SLC7A6OS	ENSG00000103061	1.10	0.33	3.36
GBP3	ENSG00000117226	2.96	0.88	3.36
KLHDC9	ENSG00000162755	4.66	1.39	3.36
SLPI	ENSG00000124107	11.00	3.27	3.36
ABCA7	ENSG00000064687	2.26	0.67	3.36
PLVAP	ENSG00000130300	9.35	2.78	3.36
TCTN2	ENSG00000168778	1.17	0.35	3.36
OGDHL	ENSG00000197444	6.32	1.88	3.36
RNF166	ENSG00000158717	2.32	0.69	3.36
HSPBAP1	ENSG00000169087	1.55	0.46	3.35
FAHD2CP	ENSG00000231584	2.93	0.87	3.35

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ARHGAP27	ENSG00000159314	3.84	1.15	3.35
AC018737.1	ENSG00000236859	1.34	0.40	3.35
SETD4	ENSG00000185917	1.28	0.38	3.35
RP11-35G9.5	ENSG00000267787	2.45	0.73	3.35
AP001258.4	ENSG00000245571	1.56	0.47	3.35
RP11-440L14.1	ENSG00000249592	2.62	0.78	3.35
ZFP36L2	ENSG00000152518	2.49	0.74	3.35
PHF11	ENSG00000136147	1.58	0.47	3.35
KAT2A	ENSG00000108773	1.78	0.53	3.35
CCL26	ENSG00000006606	6.43	1.92	3.35
RP11-799D4.4	ENSG00000266947	2.87	0.86	3.35
RNF207	ENSG00000158286	3.32	0.99	3.34
CXorf24	ENSG00000196741	1.17	0.35	3.34
ZNRD1	ENSG00000066379	1.17	0.35	3.34
RP11-600F24.7	ENSG00000260285	2.13	0.64	3.33
TRIB2	ENSG00000071575	2.89	0.87	3.33
ZNF219	ENSG00000165804	2.35	0.70	3.33
AOAH	ENSG00000136250	8.16	2.45	3.33
LPCAT3	ENSG00000111684	1.80	0.54	3.33
KRBOX4	ENSG00000147121	1.17	0.35	3.33
CCDC130	ENSG00000104957	1.22	0.37	3.33
N4BP2L1	ENSG00000139597	3.50	1.05	3.32
FAM104B	ENSG00000182518	1.15	0.35	3.32
TOR2A	ENSG00000160404	1.37	0.41	3.32
RP4-714D9.5	ENSG00000261254	2.40	0.72	3.32
TSPAN12	ENSG00000106025	4.27	1.29	3.32
C9orf9	ENSG00000165698	1.50	0.45	3.32
RP11-156E6.1	ENSG00000259623	1.66	0.50	3.32
CRABP2	ENSG00000143320	6.24	1.88	3.31
EVL	ENSG00000196405	2.05	0.62	3.31
UBA7	ENSG00000182179	1.99	0.60	3.31
RP11-262H14.1	ENSG00000238113	2.49	0.75	3.31
ENPP6	ENSG00000164303	9.92	3.00	3.31
CLIC2	ENSG00000155962	6.63	2.00	3.31
ZNF773	ENSG00000152439	1.22	0.37	3.31
ALX4	ENSG00000052850	10.92	3.30	3.31
CEBPD	ENSG00000221869	5.00	1.51	3.31
C3orf18	ENSG00000088543	1.07	0.32	3.31
NFKBID	ENSG00000167604	2.49	0.75	3.30
ABCC5	ENSG00000114770	1.05	0.32	3.30
LGALS3BP	ENSG00000108679	1.15	0.35	3.30
RP11-611E13.2	ENSG00000257815	2.08	0.63	3.30
EGFL6	ENSG00000198759	10.38	3.15	3.30
NINJ1	ENSG00000131669	2.49	0.76	3.30
DHX58	ENSG00000108771	2.14	0.65	3.30

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ADC	ENSG00000142920	3.01	0.91	3.30
SHMT1	ENSG00000176974	1.52	0.46	3.29
MRM1	ENSG00000129282	1.80	0.55	3.29
ETV5	ENSG00000244405	1.91	0.58	3.29
PCDHA11	ENSG00000249158	5.50	1.67	3.29
PPM1K	ENSG00000163644	2.03	0.62	3.29
ABHD3	ENSG00000158201	1.97	0.60	3.28
PCDHAC2	ENSG00000243232	5.48	1.67	3.28
PDCL3P4	ENSG00000244119	3.30	1.00	3.28
DLG2	ENSG00000150672	4.44	1.35	3.28
CROCCP2	ENSG00000215908	2.02	0.61	3.28
RINL	ENSG00000187994	3.76	1.15	3.28
C1orf63	ENSG00000117616	2.10	0.64	3.28
CDC14A	ENSG00000079335	2.95	0.90	3.28
PCDHA12	ENSG00000251664	5.56	1.70	3.28
CTD-2086O20.3	ENSG00000267381	2.05	0.63	3.28
TSNAXIP1	ENSG00000102904	3.10	0.95	3.28
RP11-27M15.1	ENSG00000260942	3.12	0.95	3.28
BRD8	ENSG00000112983	1.00	0.31	3.27
ZNF230	ENSG00000159882	1.58	0.48	3.27
ADCY4	ENSG00000129467	6.18	1.89	3.27
PIK3IP1	ENSG00000100100	3.67	1.12	3.27
RP11-35G9.3	ENSG00000267040	2.36	0.72	3.27
AC074117.10	ENSG00000234072	1.93	0.59	3.27
RP11-983P16.4	ENSG00000257337	3.09	0.94	3.27
GYPC	ENSG00000136732	8.71	2.67	3.27
SLC13A4	ENSG00000164707	5.87	1.80	3.27
USP21	ENSG00000143258	1.17	0.36	3.27
PPOX	ENSG00000143224	1.45	0.44	3.27
GALNT11	ENSG00000178234	1.25	0.38	3.27
CASP10	ENSG00000003400	2.55	0.78	3.27
CLK1	ENSG00000013441	1.99	0.61	3.26
TMEM218	ENSG00000150433	1.10	0.34	3.26
XXbac-BPG300A18.13	ENSG00000259382	1.83	0.56	3.26
ARFRP1	ENSG00000101246	1.16	0.36	3.26
LRRC8C	ENSG00000171488	1.69	0.52	3.26
RP4-758J18.2	ENSG00000224870	1.20	0.37	3.26
LAT2	ENSG00000086730	5.60	1.72	3.26
COMMD3	ENSG00000148444	1.09	0.33	3.26
CRYL1	ENSG00000165475	2.30	0.71	3.26
AGAP5	ENSG00000172650	1.79	0.55	3.26
LINC00263	ENSG00000235823	1.85	0.57	3.25
AD000090.2	ENSG00000236144	2.14	0.66	3.25
SPATA13	ENSG00000182957	4.63	1.42	3.25
ZNF211	ENSG00000121417	1.38	0.43	3.25

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

NDUFS7	ENSG00000115286	1.34	0.41	3.25
STAC3	ENSG00000185482	2.63	0.81	3.25
ZNF429	ENSG00000197013	1.65	0.51	3.25
FBXO24	ENSG00000106336	4.09	1.26	3.24
VCAM1	ENSG00000162692	8.14	2.51	3.24
TMEM256	ENSG00000205544	1.13	0.35	3.24
HSPA6	ENSG00000173110	6.42	1.98	3.24
FMNL1	ENSG00000184922	4.54	1.40	3.24
DIP2A	ENSG00000160305	1.50	0.46	3.24
RP11-644F5.11	ENSG00000258056	1.71	0.53	3.24
EML3	ENSG00000149499	1.42	0.44	3.24
CTC-471J1.8	ENSG00000267827	1.39	0.43	3.24
ENPP4	ENSG00000001561	1.66	0.51	3.23
RPL32P3	ENSG00000251474	1.85	0.57	3.23
MSL3	ENSG00000005302	1.05	0.32	3.23
GPX3	ENSG00000211445	7.82	2.42	3.23
RP11-85F14.5	ENSG00000239213	2.03	0.63	3.22
JAKMIP3	ENSG00000188385	4.56	1.42	3.22
NAPA-AS1	ENSG00000268061	2.23	0.69	3.22
RP11-75L1.2	ENSG00000213443	1.41	0.44	3.22
CTD-2192J16.20	ENSG00000269693	1.48	0.46	3.22
DIRC3	ENSG00000231672	4.32	1.34	3.22
THAP10	ENSG00000129028	1.07	0.33	3.22
PCDHA13	ENSG00000239389	5.45	1.69	3.22
MRPL50	ENSG00000136897	1.08	0.34	3.22
C2orf68	ENSG00000168887	1.22	0.38	3.22
AC004166.7	ENSG00000160828	1.61	0.50	3.22
STAT5A	ENSG00000126561	3.39	1.06	3.21
ARHGAP9	ENSG00000123329	4.94	1.54	3.21
PCDHAC1	ENSG00000248383	5.44	1.69	3.21
DDRGK1	ENSG00000198171	1.07	0.33	3.21
PARP14	ENSG00000173193	1.28	0.40	3.21
ARHGEF1	ENSG00000076928	1.04	0.32	3.21
ARIH2OS	ENSG00000221883	1.86	0.58	3.21
MRPS25	ENSG00000131368	1.17	0.36	3.21
LMO4	ENSG00000143013	3.64	1.13	3.21
PCDHA8	ENSG00000204962	5.42	1.69	3.20
MED9	ENSG00000141026	1.39	0.43	3.20
TSGA10	ENSG00000135951	3.20	1.00	3.20
PCDHA10	ENSG00000250120	5.26	1.64	3.20
COL27A1	ENSG00000196739	4.44	1.39	3.20
PKDCC	ENSG00000162878	4.29	1.34	3.20
CDKN1C	ENSG00000129757	5.26	1.64	3.20
LYRM9	ENSG00000232859	2.75	0.86	3.20
PCDHA3	ENSG00000255408	5.49	1.72	3.20

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

ZNF799	ENSG00000196466	1.89	0.59	3.20
COQ4	ENSG00000167113	1.47	0.46	3.20
PABPN1	ENSG00000100836	1.33	0.42	3.20
RP11-848P1.2	ENSG00000264456	3.38	1.06	3.20
IL17RC	ENSG00000163702	1.16	0.36	3.19
PCDHA9	ENSG00000204961	5.42	1.70	3.19
ZNF19	ENSG00000157429	2.02	0.63	3.19
ZNF775	ENSG00000196456	1.51	0.47	3.19
PCDHA7	ENSG00000204963	5.39	1.69	3.19
UBXN11	ENSG00000158062	1.60	0.50	3.19
SLCO2A1	ENSG00000174640	5.97	1.87	3.19
RGS14	ENSG00000169220	1.93	0.61	3.19
FIBIN	ENSG00000176971	8.50	2.67	3.19
SCARF1	ENSG00000074660	4.66	1.46	3.18
SUZ12P	ENSG00000264538	1.55	0.49	3.18
AC040173.1	ENSG00000257026	1.94	0.61	3.18
SMYD4	ENSG00000186532	1.06	0.33	3.18
AC092295.7	ENSG00000233527	1.30	0.41	3.17
CDK20	ENSG00000156345	1.82	0.57	3.17
CARD9	ENSG00000187796	2.45	0.77	3.17
FAM134C	ENSG00000141699	1.17	0.37	3.17
N4BP3	ENSG00000145911	4.61	1.45	3.17
FLT4	ENSG00000037280	5.89	1.86	3.17
PCDHA2	ENSG00000204969	5.37	1.69	3.17
RP11-488L18.10	ENSG00000259865	1.63	0.52	3.17
PDGFRL	ENSG00000104213	3.75	1.19	3.17
C11orf71	ENSG00000180425	2.01	0.64	3.17
PDK4	ENSG00000004799	8.96	2.83	3.16
ITPR1	ENSG00000150995	2.91	0.92	3.16
CTSL1	ENSG00000135047	1.71	0.54	3.16
DOK3	ENSG00000146094	2.29	0.73	3.16
AC093323.3	ENSG00000170846	1.03	0.33	3.16
JMJD7	ENSG00000243789	1.08	0.34	3.16
PCDHA4	ENSG00000204967	5.38	1.70	3.16
EPB41L2	ENSG00000079819	2.03	0.64	3.16
ARRB2	ENSG00000141480	2.66	0.84	3.16
PCDHA1	ENSG00000204970	5.33	1.69	3.16
FAM26F	ENSG00000188820	4.96	1.57	3.16
AL161915.1	ENSG00000212670	2.42	0.77	3.16
LRTOMT	ENSG00000184154	1.12	0.36	3.16
ZNF354B	ENSG00000178338	1.01	0.32	3.15
FCHO1	ENSG00000130475	5.57	1.77	3.15
RP11-473M20.14	ENSG00000263072	1.45	0.46	3.15
PUS10	ENSG00000162927	1.12	0.36	3.15
PRKCD	ENSG00000163932	2.77	0.88	3.15

List of genes more highly expressed in primary merlin-negative meningiomas than in merlin-expressing cultured arachnoidal cells

CAB39L	ENSG00000102547	4.11	1.30	3.15
SMAP2	ENSG00000084070	2.44	0.77	3.15

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

Gene Symbol	ENSEMBL ID	mean fold change	sd	Z score
ARMC9	ENSG00000135931	-3.15	0.32	-9.72
KRT17	ENSG00000128422	-10.98	1.26	-8.71
SAMD9	ENSG00000205413	-2.54	0.35	-7.24
GDA	ENSG00000119125	-11.90	1.66	-7.15
PGBD3	ENSG00000258838	-4.21	0.59	-7.11
PGBD3	ENSG00000243251	-4.09	0.58	-7.08
BACH1	ENSG00000156273	-2.20	0.32	-6.89
ERCC6	ENSG00000225830	-3.69	0.54	-6.78
PAPPA2	ENSG00000116183	-7.32	1.18	-6.21
LPP	ENSG00000145012	-1.72	0.28	-6.12
PKP1	ENSG00000081277	-10.09	1.73	-5.84
RNF168	ENSG00000163961	-1.35	0.23	-5.80
WEE1	ENSG00000166483	-2.91	0.50	-5.79
Metazoa_SRP	ENSG00000243869	-3.61	0.63	-5.73
SLC7A5	ENSG00000103257	-5.96	1.05	-5.66
SRPK1	ENSG00000096063	-2.21	0.41	-5.42
CCDC81	ENSG00000149201	-3.48	0.65	-5.37
PLXNA3	ENSG00000130827	-1.55	0.30	-5.23
C15orf62	ENSG00000188277	-6.62	1.28	-5.19
ACPL2	ENSG00000155893	-2.21	0.44	-4.97
CYB5R3	ENSG00000100243	-1.60	0.32	-4.91
RFX7	ENSG00000181827	-1.37	0.28	-4.91
ACTG2	ENSG00000163017	-7.68	1.57	-4.89
DLGAP4	ENSG00000080845	-1.61	0.33	-4.89
CEACAM19	ENSG00000186567	-2.75	0.56	-4.87
GALNT1	ENSG00000141429	-2.70	0.56	-4.85
CCDC80	ENSG00000091986	-3.06	0.63	-4.83
CTB-85P21.2	ENSG00000259787	-4.51	0.94	-4.82
ADCY9	ENSG00000162104	-1.77	0.37	-4.81
DUSP4	ENSG00000120875	-5.50	1.14	-4.81
SOGA1	ENSG00000149639	-1.82	0.38	-4.77
RDH10	ENSG00000121039	-4.06	0.86	-4.73
SMURF2	ENSG00000108854	-1.73	0.37	-4.73
LIF	ENSG00000128342	-6.92	1.48	-4.68
AL021707.2	ENSG00000257034	-1.07	0.23	-4.67
FBN1	ENSG00000166147	-2.77	0.59	-4.66
SHOC2	ENSG00000108061	-1.41	0.30	-4.65
NMD3	ENSG00000169251	-1.00	0.22	-4.64
RP11-280F2.2	ENSG00000242759	-3.06	0.66	-4.63
OXTR	ENSG00000180914	-5.75	1.25	-4.62
TMEM132D	ENSG00000151952	-11.28	2.49	-4.53
PVR	ENSG00000073008	-4.16	0.92	-4.53

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

HAS3	ENSG00000103044	-2.34	0.52	-4.52
OXSR1	ENSG00000172939	-1.30	0.29	-4.49
ABCC1	ENSG00000103222	-4.39	0.98	-4.49
KLHL5	ENSG00000109790	-3.91	0.87	-4.48
MYH9	ENSG00000100345	-3.13	0.70	-4.48
LAMC1	ENSG00000135862	-2.75	0.61	-4.47
XBP1	ENSG00000100219	-1.71	0.38	-4.47
RAP1GAP2	ENSG00000132359	-2.51	0.56	-4.47
RALGPS2	ENSG00000116191	-5.53	1.24	-4.45
CLIP1	ENSG00000130779	-1.19	0.27	-4.45
TLE4	ENSG00000106829	-3.19	0.72	-4.44
PGD	ENSG00000142657	-1.99	0.45	-4.43
PCK2	ENSG00000100889	-2.43	0.55	-4.42
FLNA	ENSG00000196924	-2.80	0.64	-4.40
PCDH7	ENSG00000169851	-11.74	2.68	-4.39
KCNK6	ENSG00000099337	-2.81	0.65	-4.35
ATXN1	ENSG00000215019	-1.32	0.31	-4.32
SLC12A6	ENSG00000140199	-2.74	0.64	-4.32
FADS3	ENSG00000221968	-1.92	0.45	-4.31
SSH1	ENSG00000084112	-1.82	0.42	-4.31
MED13	ENSG00000108510	-1.14	0.26	-4.31
ROBO2	ENSG00000185008	-8.03	1.87	-4.30
IL11	ENSG00000095752	-5.78	1.35	-4.29
GTPBP1	ENSG00000100226	-1.02	0.24	-4.29
PDIA5	ENSG00000065485	-1.90	0.44	-4.29
KRT7	ENSG00000135480	-10.99	2.57	-4.28
CREB5	ENSG00000146592	-3.76	0.88	-4.26
EP300	ENSG00000100393	-1.06	0.25	-4.24
CPEB2	ENSG00000137449	-2.99	0.71	-4.23
RP11-29G8.3	ENSG00000261553	-3.19	0.76	-4.22
LUZP2	ENSG00000187398	-11.25	2.69	-4.19
GPR156	ENSG00000175697	-2.60	0.62	-4.18
C5orf24	ENSG00000181904	-1.87	0.45	-4.18
SCAF11	ENSG00000139218	-1.95	0.47	-4.17
ZNF451	ENSG00000112200	-1.39	0.33	-4.16
VCL	ENSG00000035403	-2.49	0.60	-4.15
YARS	ENSG00000134684	-2.87	0.69	-4.14
SACS	ENSG00000151835	-3.13	0.76	-4.12
GLIPR1	ENSG00000139278	-2.68	0.65	-4.12
WARS	ENSG00000140105	-2.33	0.57	-4.10
RBFOX2	ENSG00000100320	-1.49	0.36	-4.10
PRKCA	ENSG00000154229	-2.68	0.65	-4.09
LCOR	ENSG00000196233	-1.50	0.37	-4.09
AC026806.2	ENSG00000268913	-2.37	0.58	-4.08
ALDH3A1	ENSG00000108602	-6.84	1.68	-4.08

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

AMIGO2	ENSG00000139211	-5.49	1.35	-4.07
RAMP1	ENSG00000132329	-6.58	1.62	-4.07
TMEM65	ENSG00000164983	-1.55	0.38	-4.07
FERMT2	ENSG00000073712	-2.97	0.73	-4.07
SLC6A9	ENSG00000196517	-3.54	0.87	-4.06
CACNG4	ENSG00000075461	-5.75	1.42	-4.06
THOC6	ENSG00000131652	-1.66	0.41	-4.05
MAPK1	ENSG00000100030	-1.40	0.35	-4.04
FAM69A	ENSG00000154511	-2.53	0.63	-4.04
UBE2H	ENSG00000186591	-1.02	0.25	-4.04
KDM5B	ENSG00000117139	-1.56	0.39	-4.03
SCN3A	ENSG00000153253	-10.28	2.56	-4.02
RC3H2	ENSG00000056586	-1.12	0.28	-4.02
ADAMTS1	ENSG00000154734	-4.30	1.07	-4.00
C11orf87	ENSG00000185742	-8.82	2.21	-3.99
AHR	ENSG00000106546	-4.27	1.07	-3.99
STK38L	ENSG00000211455	-2.17	0.54	-3.99
FANCE	ENSG00000112039	-3.26	0.82	-3.99
CLCF1	ENSG00000175505	-5.65	1.42	-3.98
CPNE7	ENSG00000178773	-6.91	1.74	-3.97
MAN2A1	ENSG00000112893	-2.09	0.53	-3.96
NPTN	ENSG00000156642	-1.38	0.35	-3.96
FBXO30	ENSG00000118496	-1.66	0.42	-3.95
RP11-16M8.2	ENSG00000246430	-5.51	1.40	-3.94
AC144831.1	ENSG00000261888	-4.02	1.02	-3.93
GSK3B	ENSG00000082701	-1.20	0.31	-3.93
SYNC	ENSG00000162520	-3.55	0.90	-3.93
ZNF347	ENSG00000197937	-1.96	0.50	-3.92
UBASH3B	ENSG00000154127	-4.74	1.21	-3.92
IGFBP1	ENSG00000146678	-10.96	2.80	-3.92
MTHFD1L	ENSG00000120254	-2.29	0.59	-3.89
MYOCD	ENSG00000141052	-9.34	2.40	-3.89
UGDH	ENSG00000109814	-3.80	0.98	-3.89
ANK1	ENSG00000029534	-6.38	1.64	-3.88
MAFG-AS1	ENSG00000265688	-2.24	0.58	-3.88
FAT1	ENSG00000083857	-2.75	0.71	-3.87
TGFB1I1	ENSG00000140682	-2.03	0.53	-3.87
PPP3CA	ENSG00000138814	-1.48	0.38	-3.87
CCDC50	ENSG00000152492	-1.24	0.32	-3.86
ALDH1A3	ENSG00000184254	-9.14	2.37	-3.86
KCTD16	ENSG00000183775	-5.60	1.46	-3.85
NF2	ENSG00000186575	-3.24	0.84	-3.84
STAM	ENSG00000136738	-1.53	0.40	-3.84
LOXL3	ENSG00000115318	-3.45	0.90	-3.84
TXNRD1	ENSG00000198431	-2.74	0.72	-3.83

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

SPIRE1	ENSG00000134278	-1.74	0.46	-3.81
NAP1L4P1	ENSG00000177173	-1.98	0.52	-3.81
QSOX1	ENSG00000116260	-2.55	0.67	-3.81
CD109	ENSG00000156535	-5.43	1.43	-3.81
MTHFD2	ENSG00000065911	-2.71	0.71	-3.80
DGKA	ENSG00000065357	-1.04	0.27	-3.80
GNAI1	ENSG00000127955	-2.50	0.66	-3.79
DOK1	ENSG00000115325	-1.23	0.33	-3.78
ASNS	ENSG00000070669	-2.17	0.58	-3.77
BAG2	ENSG00000112208	-3.30	0.87	-3.77
LNPEP	ENSG00000113441	-3.24	0.86	-3.77
SERAC1	ENSG00000122335	-1.80	0.48	-3.77
RP11-448G15.3	ENSG00000261490	-2.53	0.67	-3.76
SLC4A2	ENSG00000164889	-1.48	0.40	-3.74
MYADM	ENSG00000179820	-3.35	0.90	-3.72
CYP26B1	ENSG00000003137	-5.46	1.47	-3.72
VPS13A	ENSG00000197969	-2.97	0.80	-3.71
LOXL1-AS1	ENSG00000261801	-2.69	0.72	-3.71
MAP3K9	ENSG00000006432	-3.15	0.85	-3.71
SRD5A1	ENSG00000145545	-2.40	0.65	-3.70
MLF1	ENSG00000178053	-1.86	0.50	-3.70
SEC24D	ENSG00000150961	-1.73	0.47	-3.69
HCN2	ENSG00000099822	-4.59	1.24	-3.69
DGKH	ENSG00000102780	-4.83	1.31	-3.69
ERBB3	ENSG00000065361	-5.61	1.52	-3.68
ZC3H7B	ENSG00000100403	-1.42	0.38	-3.68
AC010761.8	ENSG00000264577	-9.13	2.48	-3.68
IARS	ENSG00000196305	-1.62	0.44	-3.68
FSTL1	ENSG00000163430	-1.54	0.42	-3.68
MMP1	ENSG00000196611	-10.19	2.77	-3.68
COL4A5	ENSG00000188153	-3.07	0.84	-3.66
PTPRK	ENSG00000152894	-3.82	1.05	-3.66
AKIRIN1	ENSG00000174574	-1.23	0.34	-3.65
SCARA3	ENSG00000168077	-2.48	0.68	-3.65
ADAMTS14	ENSG00000138316	-5.34	1.47	-3.64
REV3L	ENSG00000009413	-1.84	0.51	-3.63
LHX4	ENSG00000121454	-7.93	2.18	-3.63
CTTNBP2NL	ENSG00000143079	-2.10	0.58	-3.62
WNT2B	ENSG00000134245	-3.43	0.95	-3.62
DST	ENSG00000151914	-2.02	0.56	-3.62
COL1A1	ENSG00000108821	-2.54	0.70	-3.62
PVRL3	ENSG00000177707	-2.36	0.65	-3.61
AC013470.6	ENSG00000236048	-1.80	0.50	-3.61
SYNJ2	ENSG00000078269	-2.63	0.73	-3.61
TBC1D19	ENSG00000109680	-1.75	0.48	-3.61

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

BICD1	ENSG00000151746	-2.38	0.66	-3.60
PPT2	ENSG00000221988	-1.28	0.36	-3.59
MAP4	ENSG00000047849	-1.36	0.38	-3.59
AC005544.1	ENSG00000214167	-5.65	1.58	-3.59
NDFIP2	ENSG00000102471	-1.53	0.43	-3.59
HSPG2	ENSG00000142798	-1.99	0.56	-3.57
SLC36A1	ENSG00000123643	-2.57	0.72	-3.56
PPP1R12A	ENSG00000058272	-1.01	0.28	-3.56
MICALL1	ENSG00000100139	-2.90	0.82	-3.56
C1orf198	ENSG00000119280	-3.36	0.94	-3.56
GLIS3	ENSG00000107249	-5.96	1.68	-3.56
TP53BP2	ENSG00000143514	-1.06	0.30	-3.56
TCF20	ENSG00000100207	-1.19	0.34	-3.55
ACTN1	ENSG00000072110	-2.41	0.68	-3.54
JOSD1	ENSG00000100221	-1.25	0.35	-3.54
N4BP2	ENSG00000078177	-2.23	0.63	-3.54
AMPH	ENSG00000078053	-3.13	0.89	-3.53
DUSP8	ENSG00000184545	-4.28	1.21	-3.53
ARHGAP29	ENSG00000137962	-2.62	0.74	-3.52
FAM114A1	ENSG00000197712	-1.54	0.44	-3.52
NCOA7	ENSG00000111912	-2.89	0.82	-3.52
TRAM2	ENSG00000065308	-3.02	0.86	-3.51
UBE2HP1	ENSG00000253677	-2.32	0.66	-3.50
AMER1	ENSG00000184675	-1.19	0.34	-3.50
MAFG	ENSG00000197063	-1.50	0.43	-3.50
SLC16A7	ENSG00000118596	-7.62	2.18	-3.49
ACTN4	ENSG00000130402	-2.32	0.67	-3.48
ZFHX4	ENSG00000091656	-4.87	1.40	-3.48
RNF217	ENSG00000146373	-1.72	0.49	-3.48
TUBA1A	ENSG00000167552	-2.26	0.65	-3.47
ABL2	ENSG00000143322	-2.22	0.64	-3.47
SYNJ1	ENSG00000159082	-1.50	0.43	-3.47
PLEKHG4	ENSG00000196155	-2.35	0.68	-3.46
PRR14L	ENSG00000183530	-1.35	0.39	-3.46
RP1-152L7.5	ENSG00000216775	-3.63	1.05	-3.46
ZBED4	ENSG00000100426	-1.50	0.43	-3.46
MAN1A2	ENSG00000198162	-1.73	0.50	-3.46
COMT	ENSG00000093010	-1.34	0.39	-3.45
KIF5B	ENSG00000170759	-1.65	0.48	-3.45
LASP1	ENSG00000002834	-1.63	0.47	-3.45
RBM15	ENSG00000162775	-1.55	0.45	-3.44
SLC17A5	ENSG00000119899	-1.59	0.46	-3.43
PLS3	ENSG00000102024	-2.90	0.84	-3.43
PTGS2	ENSG00000073756	-6.34	1.85	-3.43
GFPT1	ENSG00000198380	-1.37	0.40	-3.42

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

DBN1	ENSG00000113758	-1.38	0.40	-3.42
SLC5A3	ENSG00000198743	-3.39	0.99	-3.42
XPO6	ENSG00000169180	-1.05	0.31	-3.41
WDR1	ENSG00000071127	-2.06	0.60	-3.41
NDEL1	ENSG00000166579	-1.05	0.31	-3.40
AC098614.2	ENSG00000213846	-2.36	0.69	-3.40
ADRB2	ENSG00000169252	-3.62	1.07	-3.40
CDC42EP1	ENSG00000128283	-2.71	0.80	-3.39
TMEM184B	ENSG00000198792	-1.50	0.44	-3.39
NEK7	ENSG00000151414	-2.28	0.67	-3.39
KIAA1586	ENSG00000168116	-1.32	0.39	-3.39
DDA1	ENSG00000130311	-1.10	0.33	-3.38
PCDH10	ENSG00000138650	-9.84	2.91	-3.38
NTN4	ENSG00000074527	-4.11	1.22	-3.38
SLC1A5	ENSG00000105281	-3.40	1.01	-3.38
AHNAK2	ENSG00000185567	-5.03	1.49	-3.37
CSRP2	ENSG00000175183	-2.25	0.67	-3.37
ARSJ	ENSG00000180801	-5.69	1.69	-3.37
RP4-671G15.3	ENSG00000248201	-1.91	0.57	-3.37
STAC	ENSG00000144681	-9.15	2.72	-3.37
LMO7	ENSG00000136153	-3.26	0.97	-3.37
RP11-360F5.3	ENSG00000249685	-3.29	0.98	-3.37
RGS4	ENSG00000117152	-8.02	2.39	-3.36
SLC4A7	ENSG00000033867	-2.72	0.81	-3.36
MTMR2	ENSG00000087053	-1.16	0.35	-3.35
SYT1	ENSG00000067715	-7.77	2.32	-3.35
CAPN5	ENSG00000149260	-2.75	0.82	-3.35
KLF6	ENSG00000067082	-2.48	0.74	-3.35
BDNF	ENSG00000176697	-9.97	2.98	-3.35
NEK10	ENSG00000163491	-3.77	1.13	-3.34
LOC124685	ENSG00000228118	-2.24	0.67	-3.34
THOC5	ENSG00000100296	-1.51	0.45	-3.34
PDLIM5	ENSG00000163110	-2.36	0.71	-3.34
TSHZ3	ENSG00000121297	-1.70	0.51	-3.34
COL4A1	ENSG00000187498	-4.03	1.21	-3.34
IPO5	ENSG00000065150	-1.63	0.49	-3.34
EPRS	ENSG00000136628	-1.64	0.49	-3.33
GS1-44D20.1	ENSG00000254332	-2.66	0.80	-3.33
COL5A2	ENSG00000204262	-2.81	0.84	-3.32
FAM132B	ENSG00000178752	-6.88	2.07	-3.32
CTIF	ENSG00000134030	-1.56	0.47	-3.32
TUFT1	ENSG00000143367	-3.19	0.96	-3.32
C22orf29	ENSG00000215012	-1.84	0.56	-3.31
PITPNB	ENSG00000180957	-1.73	0.52	-3.31
RICTOR	ENSG00000164327	-1.24	0.38	-3.29

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

MICAL3	ENSG00000243156	-1.77	0.54	-3.29
RIMS1	ENSG00000079841	-7.90	2.41	-3.29
RP11-333E13.2	ENSG00000250568	-1.70	0.52	-3.28
TEAD1	ENSG00000187079	-1.36	0.42	-3.28
TFAP2A	ENSG00000137203	-5.43	1.65	-3.28
PPRC1	ENSG00000148840	-1.36	0.41	-3.28
ASB1	ENSG00000065802	-1.57	0.48	-3.28
ACTG1	ENSG00000184009	-1.52	0.46	-3.28
COL4A2	ENSG00000134871	-3.77	1.15	-3.28
LIMS1	ENSG00000169756	-1.64	0.50	-3.27
RP11-145M9.3	ENSG00000181260	-3.15	0.97	-3.27
PGM2L1	ENSG00000165434	-2.47	0.76	-3.26
AL021977.1	ENSG00000256873	-1.58	0.49	-3.26
DUSP5	ENSG00000138166	-5.06	1.56	-3.26
SGIP1	ENSG00000118473	-4.03	1.24	-3.25
TRIB1	ENSG00000173334	-4.13	1.28	-3.24
CYP51A1	ENSG00000001630	-1.41	0.43	-3.24
VPS13B	ENSG00000132549	-1.31	0.41	-3.23
IGF2BP3	ENSG00000136231	-6.94	2.15	-3.23
MYL12A	ENSG00000101608	-1.63	0.51	-3.22
LRRD1	ENSG00000240720	-1.39	0.43	-3.22
INHBA	ENSG00000122641	-5.24	1.63	-3.21
CSRP1	ENSG00000159176	-1.51	0.47	-3.21
PGRMC2	ENSG00000164040	-1.19	0.37	-3.20
MSNP1	ENSG00000251593	-1.55	0.48	-3.20
USP13	ENSG00000058056	-2.21	0.69	-3.20
TPM1	ENSG00000140416	-2.17	0.68	-3.20
DHRS9	ENSG00000073737	-5.47	1.71	-3.20
EDIL3	ENSG00000164176	-7.27	2.28	-3.19
TERT	ENSG00000164362	-10.58	3.32	-3.18
GPRC5A	ENSG00000013588	-6.20	1.95	-3.18
ODC1	ENSG00000115758	-1.78	0.56	-3.18
EPHA5	ENSG00000145242	-11.75	3.70	-3.18
ZNF469	ENSG00000225614	-2.66	0.84	-3.17
ENTPD7	ENSG00000198018	-2.27	0.72	-3.17
FMR1	ENSG00000102081	-1.07	0.34	-3.17
PDLIM3	ENSG00000154553	-4.23	1.33	-3.17
DPY19L1	ENSG00000173852	-1.26	0.40	-3.17
TCF7	ENSG00000081059	-3.26	1.03	-3.17
CTD-3252C9.4	ENSG00000267519	-3.25	1.03	-3.16
PALLD	ENSG00000129116	-3.51	1.11	-3.16
KCNH1	ENSG00000143473	-6.21	1.96	-3.16
OSR2	ENSG00000164920	-8.36	2.65	-3.16
AVEN	ENSG00000169857	-1.54	0.49	-3.16
ADAMTS8	ENSG00000134917	-7.68	2.43	-3.16

List of genes more highly expressed in merlin-expressing cultured arachnoidal cells than in primary merlin-negative meningiomas

TUBA4A	ENSG00000127824	-3.25	1.03	-3.16
RBMS2	ENSG00000076067	-1.21	0.38	-3.16
DSEL	ENSG00000171451	-1.77	0.56	-3.15
CSGALNACT2	ENSG00000169826	-1.16	0.37	-3.15

List of genes robustly upregulated by *NF2* inactivation in cultured arachnoidal cells in our expanded data set

Gene Symbol	Ensembl ID	logFC	logCPM	F	PValue	Benjamini-Hochberg P value	Bonferroni P value
TPTEP1	ENSG00000100181	14.65	4.44	1039.25	2.40E-22	3.70E-18	3.70E-18
PNPLA4	ENSG00000006757	12.56	3.50	858.24	2.65E-21	1.36E-17	4.08E-17
CACNA1A	ENSG00000141837	5.43	2.98	462.61	7.58E-19	1.67E-15	1.17E-14
KHDRBS3	ENSG00000131773	3.83	1.46	436.60	1.62E-18	3.12E-15	2.50E-14
RNF182	ENSG00000180537	5.25	4.52	354.65	2.41E-17	3.72E-14	3.72E-13
C1orf21	ENSG00000116667	6.27	2.80	328.13	6.55E-17	9.19E-14	1.01E-12
ZNF516	ENSG00000101493	7.55	3.07	321.06	8.67E-17	1.11E-13	1.34E-12
CDCA7L	ENSG00000164649	2.04	5.92	288.38	3.41E-16	4.04E-13	5.25E-12
LPCAT2	ENSG00000087253	8.39	3.12	250.36	2.03E-15	1.78E-12	3.13E-11
CDH13	ENSG00000140945	3.18	5.76	232.85	5.02E-15	3.87E-12	7.74E-11
ENOX1	ENSG00000120658	4.21	1.98	215.03	1.35E-14	8.67E-12	2.08E-10
SGK223	ENSG00000182319	4.16	5.41	212.69	1.54E-14	9.37E-12	2.38E-10
MFAP3L	ENSG00000198948	4.43	4.41	212.27	1.58E-14	9.37E-12	2.44E-10
TMEM178B	ENSG00000261115	3.06	5.62	205.69	2.33E-14	1.19E-11	3.59E-10
OSBPL3	ENSG00000070882	1.78	5.32	186.26	7.82E-14	3.35E-11	1.21E-09
PSG1	ENSG00000231924	8.24	3.49	175.92	1.56E-13	6.17E-11	2.41E-09
EBF2	ENSG00000221818	2.99	3.88	171.78	2.08E-13	7.81E-11	3.20E-09
PRUNE2	ENSG00000106772	3.94	4.43	159.42	5.07E-13	1.79E-10	7.82E-09
EPHA4	ENSG00000116106	3.00	3.68	159.31	5.11E-13	1.79E-10	7.88E-09
CNNM1	ENSG00000119946	7.69	-0.02	155.43	6.85E-13	2.20E-10	1.06E-08
TRIM58	ENSG00000162722	4.04	4.95	144.70	1.59E-12	4.32E-10	2.45E-08
KIAA1244	ENSG00000112379	2.61	4.43	144.25	1.65E-12	4.32E-10	2.55E-08
ANKRD18B	ENSG00000230453	8.15	-0.56	154.57	2.18E-12	5.43E-10	3.36E-08
FRMD4B	ENSG00000114541	6.48	2.80	133.68	4.01E-12	9.36E-10	6.17E-08
PODXL2	ENSG00000114631	4.72	3.28	131.80	4.72E-12	1.07E-09	7.27E-08
TRPV2	ENSG00000187688	5.37	1.93	131.49	4.85E-12	1.08E-09	7.48E-08
LZTS1	ENSG00000061337	2.22	4.60	123.11	1.03E-11	2.15E-09	1.59E-07
PTPRF	ENSG00000142949	2.46	6.67	120.03	1.38E-11	2.72E-09	2.12E-07
MIR137HG	ENSG00000225206	4.35	2.07	120.02	1.38E-11	2.72E-09	2.12E-07
DNALI1	ENSG00000163879	4.65	0.14	118.46	1.60E-11	3.12E-09	2.47E-07
MMP2	ENSG00000087245	5.22	4.83	118.15	1.65E-11	3.13E-09	2.54E-07
STXBP6	ENSG00000168952	2.34	3.85	114.77	2.29E-11	4.19E-09	3.52E-07
FLJ14082	ENSG00000229689	2.76	0.93	113.86	2.50E-11	4.53E-09	3.85E-07
ANKFN1	ENSG00000153930	5.76	-0.73	121.96	2.90E-11	5.17E-09	4.47E-07
THRB	ENSG00000151090	4.34	2.63	112.30	2.92E-11	5.17E-09	4.50E-07
OR2W3	ENSG00000238243	3.98	2.33	109.68	3.80E-11	6.66E-09	5.86E-07
PTN	ENSG00000105894	3.54	2.39	108.07	4.48E-11	7.60E-09	6.91E-07
LAMA1	ENSG00000101680	3.70	5.36	107.49	4.76E-11	7.98E-09	7.34E-07
PCLO	ENSG00000186472	2.80	4.92	104.78	6.32E-11	1.00E-08	9.75E-07
FRMD3	ENSG00000172159	4.83	2.57	104.01	6.86E-11	1.07E-08	1.06E-06
AC108142.1	ENSG00000177822	5.07	1.35	102.66	7.92E-11	1.20E-08	1.22E-06
ZNF681	ENSG00000196172	2.99	1.07	97.57	1.38E-10	1.94E-08	2.13E-06
PSG4	ENSG00000243137	4.33	3.39	90.93	2.97E-10	3.78E-08	4.57E-06
SCRN1	ENSG00000136193	2.13	6.52	90.22	3.22E-10	4.01E-08	4.97E-06
RP11-366M4.11	ENSG00000248632	1.89	2.01	88.75	3.85E-10	4.68E-08	5.93E-06
ST3GAL6	ENSG00000064225	3.56	0.58	88.74	3.85E-10	4.68E-08	5.94E-06
LOXL2	ENSG00000134013	1.24	8.82	106.21	3.96E-10	4.77E-08	6.10E-06

List of genes robustly upregulated by *NF2* inactivation in cultured arachnoidal cells in our expanded data set

NRG1	ENSG00000157168	4.47	4.19	88.17	4.13E-10	4.93E-08	6.36E-06
GPR126	ENSG00000112414	3.47	2.37	87.28	4.60E-10	5.37E-08	7.09E-06
FAM160A1	ENSG00000164142	2.66	3.20	86.63	4.98E-10	5.72E-08	7.67E-06
AP1M2	ENSG00000129354	3.42	2.06	86.44	5.09E-10	5.82E-08	7.85E-06
GALM	ENSG00000143891	5.10	3.15	84.14	6.78E-10	7.46E-08	1.04E-05
CTSC	ENSG00000109861	1.92	8.14	82.90	7.93E-10	8.54E-08	1.22E-05
GDF6	ENSG00000156466	3.21	5.75	82.71	8.12E-10	8.69E-08	1.25E-05
PSD3	ENSG00000156011	1.42	6.41	80.94	1.02E-09	1.08E-07	1.57E-05
PDE1C	ENSG00000154678	4.98	7.18	79.40	1.24E-09	1.28E-07	1.92E-05
B4GALT6	ENSG00000118276	2.19	3.56	77.74	1.55E-09	1.52E-07	2.39E-05
PAGE5	ENSG00000158639	3.95	0.89	77.21	1.66E-09	1.59E-07	2.56E-05
MYO5B	ENSG00000167306	2.38	3.00	76.98	1.71E-09	1.61E-07	2.64E-05
CTB-175P5.4	ENSG00000269416	5.95	0.60	76.66	1.79E-09	1.65E-07	2.76E-05
GPR85	ENSG00000164604	2.36	1.03	76.45	1.84E-09	1.69E-07	2.84E-05
GBX2	ENSG00000168505	3.62	2.54	74.03	2.56E-09	2.26E-07	3.95E-05
PLK2	ENSG00000145632	1.28	8.76	70.07	4.47E-09	3.75E-07	6.89E-05
MCTP1	ENSG00000175471	3.60	2.26	69.15	5.11E-09	4.19E-07	7.88E-05
ZNF662	ENSG00000182983	4.38	0.24	69.07	5.17E-09	4.20E-07	7.97E-05
HRK	ENSG00000135116	3.65	0.98	68.96	5.25E-09	4.24E-07	8.09E-05
CCBE1	ENSG00000183287	2.29	6.30	68.17	5.89E-09	4.68E-07	9.09E-05
RP11-86A5.1	ENSG00000233403	9.23	-1.31	92.96	6.54E-09	5.12E-07	1.01E-04
MPP1	ENSG00000130830	3.92	4.47	67.31	6.69E-09	5.18E-07	1.03E-04
RP11-25K19.1	ENSG00000167912	2.98	0.70	67.23	6.76E-09	5.21E-07	1.04E-04
AOX1	ENSG00000138356	1.68	5.69	67.07	6.93E-09	5.31E-07	1.07E-04
KIRREL3	ENSG00000149571	1.18	5.17	71.08	7.76E-09	5.93E-07	1.20E-04
CACHD1	ENSG00000158966	2.86	2.13	65.00	9.45E-09	7.04E-07	1.46E-04
CADM1	ENSG00000182985	2.01	3.44	64.61	1.00E-08	7.37E-07	1.55E-04
C8orf47	ENSG00000177459	4.46	0.29	62.98	1.29E-08	9.20E-07	1.99E-04
HBEGF	ENSG00000113070	3.01	5.99	62.93	1.30E-08	9.24E-07	2.00E-04
PAG1	ENSG00000076641	2.42	4.26	62.80	1.33E-08	9.35E-07	2.04E-04
RAB11FIP1	ENSG00000156675	1.72	7.82	62.79	1.33E-08	9.35E-07	2.05E-04
CCNJL	ENSG00000135083	2.49	2.41	60.78	1.82E-08	1.23E-06	2.81E-04
MGAM	ENSG00000257335	3.93	1.35	59.91	2.09E-08	1.38E-06	3.23E-04
CXADRP3	ENSG00000265766	2.74	1.51	63.21	2.13E-08	1.40E-06	3.28E-04
LONRF3	ENSG00000175556	8.49	0.31	67.10	2.24E-08	1.45E-06	3.45E-04
SNAPC1	ENSG00000023608	1.43	7.70	58.30	2.72E-08	1.71E-06	4.19E-04
CGB7	ENSG00000196337	2.14	0.62	58.30	2.72E-08	1.71E-06	4.19E-04
OPN3	ENSG00000054277	1.24	4.14	63.47	2.79E-08	1.75E-06	4.31E-04
TRIM61	ENSG00000183439	1.64	1.77	88.85	2.85E-08	1.77E-06	4.40E-04
FAM212B	ENSG00000197852	1.96	4.06	57.57	3.07E-08	1.89E-06	4.73E-04
AP1S3	ENSG00000152056	1.23	4.50	57.19	3.26E-08	1.99E-06	5.03E-04
DYSF	ENSG00000135636	2.49	5.87	55.81	4.11E-08	2.47E-06	6.34E-04
PSG2	ENSG00000242221	6.64	-0.26	55.65	4.22E-08	2.52E-06	6.51E-04
SEMA7A	ENSG00000138623	2.41	6.65	54.60	5.05E-08	2.95E-06	7.79E-04
IL7R	ENSG00000168685	5.83	1.87	54.22	5.39E-08	3.14E-06	8.31E-04
NES	ENSG00000132688	2.75	3.85	54.08	5.52E-08	3.16E-06	8.51E-04
KIF5C	ENSG00000168280	1.49	5.60	53.81	5.79E-08	3.31E-06	8.93E-04
MPP6	ENSG00000105926	1.37	3.13	81.79	6.50E-08	3.66E-06	1.00E-03
TGIF2LX	ENSG00000153779	5.15	-1.88	55.91	6.51E-08	3.66E-06	1.00E-03
OXCT2P1	ENSG00000237624	5.16	-2.02	53.12	6.52E-08	3.66E-06	1.01E-03

List of genes robustly upregulated by *NF2* inactivation in cultured arachnoidal cells in our expanded data set

KCNJ2	ENSG00000123700	2.62	2.79	52.73	6.99E-08	3.88E-06	1.08E-03
RHBDF2	ENSG00000129667	1.66	4.07	52.70	7.02E-08	3.88E-06	1.08E-03
CD163L1	ENSG00000177675	3.79	1.67	52.62	7.12E-08	3.92E-06	1.10E-03
STARD13	ENSG00000133121	1.04	6.18	67.07	7.25E-08	3.98E-06	1.12E-03
RP11-245M24.1	ENSG00000229563	3.48	0.30	52.21	7.65E-08	4.14E-06	1.18E-03
EPHB1	ENSG00000154928	2.74	2.87	52.21	7.65E-08	4.14E-06	1.18E-03
MYO1D	ENSG00000176658	4.27	2.06	52.16	7.72E-08	4.16E-06	1.19E-03
RP11-297P16.4	ENSG00000250920	5.59	1.88	51.82	8.20E-08	4.37E-06	1.26E-03
DKK3	ENSG00000050165	1.06	8.79	99.12	9.56E-08	5.03E-06	1.47E-03
GCNT2	ENSG00000111846	2.69	2.24	50.74	9.95E-08	5.22E-06	1.53E-03
WDR66	ENSG00000158023	2.25	1.82	50.40	1.06E-07	5.47E-06	1.63E-03
CTH	ENSG00000116761	1.66	3.15	50.03	1.13E-07	5.77E-06	1.74E-03
SHC3	ENSG00000148082	5.61	-0.73	49.89	1.16E-07	5.90E-06	1.79E-03
ADCY2	ENSG00000078295	2.20	-0.19	49.38	1.27E-07	6.33E-06	1.96E-03
DTX2	ENSG00000091073	1.16	4.20	77.54	1.35E-07	6.60E-06	2.08E-03
TPST2	ENSG00000128294	1.14	4.46	67.57	1.36E-07	6.63E-06	2.10E-03
BEND7	ENSG00000165626	1.58	3.38	47.92	1.67E-07	8.02E-06	2.57E-03
ADRB1	ENSG00000043591	2.25	0.83	45.83	2.48E-07	1.16E-05	3.82E-03
SIM1	ENSG00000112246	2.22	3.31	47.80	2.56E-07	1.19E-05	3.95E-03
SOX6	ENSG00000110693	2.42	1.83	45.46	2.66E-07	1.22E-05	4.11E-03
SEPT6	ENSG00000125354	1.03	5.55	53.26	2.74E-07	1.25E-05	4.23E-03
CDH10	ENSG00000040731	10.20	-1.03	47.36	2.78E-07	1.26E-05	4.28E-03
ANKRD20A5P	ENSG00000186481	1.84	2.67	45.03	2.89E-07	1.31E-05	4.46E-03
CADM3	ENSG00000162706	3.50	4.35	44.19	3.41E-07	1.52E-05	5.26E-03
MARCH4	ENSG00000144583	2.13	4.93	43.03	4.30E-07	1.86E-05	6.62E-03
SH2D5	ENSG00000189410	2.44	3.66	42.96	4.36E-07	1.87E-05	6.72E-03
OTOGL	ENSG00000165899	2.16	0.16	42.72	4.57E-07	1.96E-05	7.04E-03
ANKRD18A	ENSG00000180071	4.07	-0.47	44.09	5.05E-07	2.15E-05	7.79E-03
CCRN4L	ENSG00000151014	1.14	5.22	42.18	5.10E-07	2.16E-05	7.86E-03
FRMD5	ENSG00000171877	1.43	3.54	41.53	5.81E-07	2.39E-05	8.96E-03
LINC00839	ENSG00000185904	1.53	3.83	41.50	5.85E-07	2.40E-05	9.01E-03
SRPX2	ENSG00000102359	2.06	1.08	41.40	5.97E-07	2.44E-05	9.20E-03
DUSP14	ENSG00000161326	0.95	6.90	42.92	6.02E-07	2.45E-05	9.28E-03
AC003051.1	ENSG00000227517	4.94	-2.27	41.05	6.42E-07	2.59E-05	9.89E-03
CTC-347C20.2	ENSG00000248371	2.74	0.05	40.83	6.72E-07	2.68E-05	1.04E-02
C10orf35	ENSG00000171224	1.73	1.43	40.70	6.91E-07	2.75E-05	1.06E-02
SDC1	ENSG00000115884	1.61	5.47	40.55	7.11E-07	2.82E-05	1.10E-02
STK40	ENSG00000196182	0.96	6.00	65.43	7.38E-07	2.90E-05	1.14E-02
RAB3B	ENSG00000169213	1.37	8.53	40.13	7.77E-07	3.05E-05	1.20E-02
SLC38A5	ENSG00000017483	2.51	-1.45	39.94	8.08E-07	3.15E-05	1.25E-02
NTF4	ENSG00000225950	2.37	-0.55	39.89	8.16E-07	3.16E-05	1.26E-02
PSG8	ENSG00000124467	6.86	-1.29	41.42	8.44E-07	3.25E-05	1.30E-02
CLMN	ENSG00000165959	1.49	4.44	39.66	8.58E-07	3.28E-05	1.32E-02
MAST4	ENSG00000069020	1.26	3.01	42.13	8.83E-07	3.35E-05	1.36E-02
FTSJ1	ENSG00000068438	0.95	5.90	50.62	9.20E-07	3.47E-05	1.42E-02
ANKRD30BP1	ENSG00000175302	3.18	-0.31	39.23	9.38E-07	3.51E-05	1.45E-02
POTEC	ENSG00000183206	2.52	2.01	38.95	9.96E-07	3.72E-05	1.54E-02
APLN	ENSG00000171388	2.42	0.84	38.73	1.04E-06	3.87E-05	1.61E-02
VEPH1	ENSG00000197415	3.72	0.55	38.58	1.08E-06	3.95E-05	1.66E-02
MATN2	ENSG00000132561	1.20	6.17	38.47	1.10E-06	4.01E-05	1.70E-02

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POLR3G	ENSG00000113356	1.28	3.05	38.46	1.11E-06	4.01E-05	1.71E-02
FAM133A	ENSG00000179083	1.85	1.53	38.42	1.12E-06	4.03E-05	1.72E-02
PORCN	ENSG00000102312	1.63	5.02	38.38	1.12E-06	4.05E-05	1.73E-02
PRPS1	ENSG00000147224	0.99	7.12	38.21	1.17E-06	4.19E-05	1.80E-02
NIPAL3	ENSG00000001461	0.94	7.57	45.73	1.20E-06	4.30E-05	1.85E-02
MYO7B	ENSG00000169994	3.67	0.24	37.96	1.23E-06	4.39E-05	1.90E-02
PSG5	ENSG00000204941	3.21	3.35	37.87	1.26E-06	4.44E-05	1.94E-02
PRSS23	ENSG00000150687	1.09	9.66	37.77	1.28E-06	4.52E-05	1.98E-02
MMP1	ENSG00000196611	6.76	7.44	37.75	1.29E-06	4.53E-05	1.99E-02
CTNNAL1	ENSG00000119326	0.92	6.93	73.46	1.31E-06	4.59E-05	2.02E-02
LY6K	ENSG00000160886	2.28	2.37	37.60	1.33E-06	4.64E-05	2.06E-02
TNFRSF11A	ENSG00000141655	2.46	2.12	37.28	1.43E-06	4.93E-05	2.20E-02
ITGA6	ENSG00000091409	1.58	7.58	37.26	1.43E-06	4.94E-05	2.21E-02
SLAMF7	ENSG00000026751	4.59	3.35	37.18	1.46E-06	5.02E-05	2.25E-02
MOK	ENSG00000080823	1.60	5.60	37.12	1.48E-06	5.07E-05	2.28E-02
EMB	ENSG00000170571	1.40	4.02	36.14	1.84E-06	6.19E-05	2.83E-02
RNF144B	ENSG00000137393	1.25	4.89	35.92	1.93E-06	6.45E-05	2.97E-02
GALNT7	ENSG00000109586	0.94	5.54	47.91	1.97E-06	6.57E-05	3.04E-02
CDH4	ENSG00000179242	9.34	0.75	38.83	2.02E-06	6.72E-05	3.12E-02
TRIM36	ENSG00000152503	1.51	3.55	35.69	2.03E-06	6.73E-05	3.13E-02
PPP2R2B	ENSG00000156475	4.63	2.18	37.03	2.06E-06	6.78E-05	3.17E-02
PAQR5	ENSG00000137819	1.28	4.73	35.62	2.06E-06	6.79E-05	3.18E-02
RP11-14N7.2	ENSG00000232527	2.04	0.89	35.60	2.07E-06	6.81E-05	3.20E-02
FERMT1	ENSG00000101311	1.38	1.52	35.60	2.14E-06	6.98E-05	3.30E-02
ZNF804A	ENSG00000170396	2.01	2.54	35.38	2.18E-06	7.07E-05	3.36E-02
NUAK2	ENSG00000163545	1.30	5.90	35.27	2.23E-06	7.22E-05	3.44E-02
TOX	ENSG00000198846	3.71	1.99	34.95	2.40E-06	7.72E-05	3.70E-02
MAGEH1	ENSG00000187601	1.18	3.18	57.54	2.49E-06	7.94E-05	3.84E-02
EDN1	ENSG00000078401	1.82	4.68	34.78	2.50E-06	7.95E-05	3.85E-02
FJX1	ENSG00000179431	1.91	4.03	34.41	2.72E-06	8.55E-05	4.19E-02
RP4-773A18.4	ENSG00000227811	1.54	0.27	38.10	2.79E-06	8.75E-05	4.30E-02
SPATA13	ENSG00000182957	1.11	3.64	35.61	2.81E-06	8.82E-05	4.34E-02
CLCN4	ENSG00000073464	1.37	5.40	34.09	2.92E-06	9.08E-05	4.50E-02
MYLK	ENSG00000065534	1.51	5.33	34.07	2.94E-06	9.11E-05	4.53E-02

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Gene Symbol	ENSEMBL ID	mean fold change	sd	Z score
ARMC9	ENSG00000135931	-3.15	0.32	-9.72
KRT17	ENSG00000128422	-10.98	1.26	-8.71
SAMD9	ENSG00000205413	-2.54	0.35	-7.24
GDA	ENSG00000119125	-11.90	1.66	-7.15
PGBD3	ENSG00000258838	-4.21	0.59	-7.11
PGBD3	ENSG00000243251	-4.09	0.58	-7.08
BACH1	ENSG00000156273	-2.20	0.32	-6.89
ERCC6	ENSG00000225830	-3.69	0.54	-6.78
PAPPA2	ENSG00000116183	-7.32	1.18	-6.21
LPP	ENSG00000145012	-1.72	0.28	-6.12
PKP1	ENSG00000081277	-10.09	1.73	-5.84
RNF168	ENSG00000163961	-1.35	0.23	-5.80
WEE1	ENSG00000166483	-2.91	0.50	-5.79
Metazoa_SRP	ENSG00000243869	-3.61	0.63	-5.73
SLC7A5	ENSG00000103257	-5.96	1.05	-5.66
SRPK1	ENSG00000096063	-2.21	0.41	-5.42
CCDC81	ENSG00000149201	-3.48	0.65	-5.37
PLXNA3	ENSG00000130827	-1.55	0.30	-5.23
C15orf62	ENSG00000188277	-6.62	1.28	-5.19
ACPL2	ENSG00000155893	-2.21	0.44	-4.97
CYB5R3	ENSG00000100243	-1.60	0.32	-4.91
RFX7	ENSG00000181827	-1.37	0.28	-4.91
ACTG2	ENSG00000163017	-7.68	1.57	-4.89
DLGAP4	ENSG00000080845	-1.61	0.33	-4.89
CEACAM19	ENSG00000186567	-2.75	0.56	-4.87
GALNT1	ENSG00000141429	-2.70	0.56	-4.85
CCDC80	ENSG00000091986	-3.06	0.63	-4.83
CTB-85P21.2	ENSG00000259787	-4.51	0.94	-4.82
ADCY9	ENSG00000162104	-1.77	0.37	-4.81
DUSP4	ENSG00000120875	-5.50	1.14	-4.81
SOGA1	ENSG00000149639	-1.82	0.38	-4.77
RDH10	ENSG00000121039	-4.06	0.86	-4.73
SMURF2	ENSG00000108854	-1.73	0.37	-4.73
LIF	ENSG00000128342	-6.92	1.48	-4.68
AL021707.2	ENSG00000257034	-1.07	0.23	-4.67
FBN1	ENSG00000166147	-2.77	0.59	-4.66
SHOC2	ENSG00000108061	-1.41	0.30	-4.65
NMD3	ENSG00000169251	-1.00	0.22	-4.64
RP11-280F2.2	ENSG00000242759	-3.06	0.66	-4.63
OXTR	ENSG00000180914	-5.75	1.25	-4.62
TMEM132D	ENSG00000151952	-11.28	2.49	-4.53
PVR	ENSG00000073008	-4.16	0.92	-4.53

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HAS3	ENSG00000103044	-2.34	0.52	-4.52
OXSR1	ENSG00000172939	-1.30	0.29	-4.49
ABCC1	ENSG00000103222	-4.39	0.98	-4.49
KLHL5	ENSG00000109790	-3.91	0.87	-4.48
MYH9	ENSG00000100345	-3.13	0.70	-4.48
LAMC1	ENSG00000135862	-2.75	0.61	-4.47
XBP1	ENSG00000100219	-1.71	0.38	-4.47
RAP1GAP2	ENSG00000132359	-2.51	0.56	-4.47
RALGPS2	ENSG00000116191	-5.53	1.24	-4.45
CLIP1	ENSG00000130779	-1.19	0.27	-4.45
TLE4	ENSG00000106829	-3.19	0.72	-4.44
PGD	ENSG00000142657	-1.99	0.45	-4.43
PCK2	ENSG00000100889	-2.43	0.55	-4.42
FLNA	ENSG00000196924	-2.80	0.64	-4.40
PCDH7	ENSG00000169851	-11.74	2.68	-4.39
KCNK6	ENSG00000099337	-2.81	0.65	-4.35
ATXN1	ENSG00000215019	-1.32	0.31	-4.32
SLC12A6	ENSG00000140199	-2.74	0.64	-4.32
FADS3	ENSG00000221968	-1.92	0.45	-4.31
SSH1	ENSG00000084112	-1.82	0.42	-4.31
MED13	ENSG00000108510	-1.14	0.26	-4.31
ROBO2	ENSG00000185008	-8.03	1.87	-4.30
IL11	ENSG00000095752	-5.78	1.35	-4.29
GTPBP1	ENSG00000100226	-1.02	0.24	-4.29
PDIA5	ENSG00000065485	-1.90	0.44	-4.29
KRT7	ENSG00000135480	-10.99	2.57	-4.28
CREB5	ENSG00000146592	-3.76	0.88	-4.26
EP300	ENSG00000100393	-1.06	0.25	-4.24
CPEB2	ENSG00000137449	-2.99	0.71	-4.23
RP11-29G8.3	ENSG00000261553	-3.19	0.76	-4.22
LUZP2	ENSG00000187398	-11.25	2.69	-4.19
GPR156	ENSG00000175697	-2.60	0.62	-4.18
C5orf24	ENSG00000181904	-1.87	0.45	-4.18
SCAF11	ENSG00000139218	-1.95	0.47	-4.17
ZNF451	ENSG00000112200	-1.39	0.33	-4.16
VCL	ENSG00000035403	-2.49	0.60	-4.15
YARS	ENSG00000134684	-2.87	0.69	-4.14
SACS	ENSG00000151835	-3.13	0.76	-4.12
GLIPR1	ENSG00000139278	-2.68	0.65	-4.12
WARS	ENSG00000140105	-2.33	0.57	-4.10
RBFOX2	ENSG00000100320	-1.49	0.36	-4.10
PRKCA	ENSG00000154229	-2.68	0.65	-4.09
LCOR	ENSG00000196233	-1.50	0.37	-4.09
AC026806.2	ENSG00000268913	-2.37	0.58	-4.08
ALDH3A1	ENSG00000108602	-6.84	1.68	-4.08

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AMIGO2	ENSG00000139211	-5.49	1.35	-4.07
RAMP1	ENSG00000132329	-6.58	1.62	-4.07
TMEM65	ENSG00000164983	-1.55	0.38	-4.07
FERMT2	ENSG00000073712	-2.97	0.73	-4.07
SLC6A9	ENSG00000196517	-3.54	0.87	-4.06
CACNG4	ENSG00000075461	-5.75	1.42	-4.06
THOC6	ENSG00000131652	-1.66	0.41	-4.05
MAPK1	ENSG00000100030	-1.40	0.35	-4.04
FAM69A	ENSG00000154511	-2.53	0.63	-4.04
UBE2H	ENSG00000186591	-1.02	0.25	-4.04
KDM5B	ENSG00000117139	-1.56	0.39	-4.03
SCN3A	ENSG00000153253	-10.28	2.56	-4.02
RC3H2	ENSG00000056586	-1.12	0.28	-4.02
ADAMTS1	ENSG00000154734	-4.30	1.07	-4.00
C11orf87	ENSG00000185742	-8.82	2.21	-3.99
AHR	ENSG00000106546	-4.27	1.07	-3.99
STK38L	ENSG00000211455	-2.17	0.54	-3.99
FANCE	ENSG00000112039	-3.26	0.82	-3.99
CLCF1	ENSG00000175505	-5.65	1.42	-3.98
CPNE7	ENSG00000178773	-6.91	1.74	-3.97
MAN2A1	ENSG00000112893	-2.09	0.53	-3.96
NPTN	ENSG00000156642	-1.38	0.35	-3.96
FBXO30	ENSG00000118496	-1.66	0.42	-3.95
RP11-16M8.2	ENSG00000246430	-5.51	1.40	-3.94
AC144831.1	ENSG00000261888	-4.02	1.02	-3.93
GSK3B	ENSG00000082701	-1.20	0.31	-3.93
SYNC	ENSG00000162520	-3.55	0.90	-3.93
ZNF347	ENSG00000197937	-1.96	0.50	-3.92
UBASH3B	ENSG00000154127	-4.74	1.21	-3.92
IGFBP1	ENSG00000146678	-10.96	2.80	-3.92
MTHFD1L	ENSG00000120254	-2.29	0.59	-3.89
MYOCD	ENSG00000141052	-9.34	2.40	-3.89
UGDH	ENSG00000109814	-3.80	0.98	-3.89
ANK1	ENSG00000029534	-6.38	1.64	-3.88
MAFG-AS1	ENSG00000265688	-2.24	0.58	-3.88
FAT1	ENSG00000083857	-2.75	0.71	-3.87
TGFB1I1	ENSG00000140682	-2.03	0.53	-3.87
PPP3CA	ENSG00000138814	-1.48	0.38	-3.87
CCDC50	ENSG00000152492	-1.24	0.32	-3.86
ALDH1A3	ENSG00000184254	-9.14	2.37	-3.86
KCTD16	ENSG00000183775	-5.60	1.46	-3.85
NF2	ENSG00000186575	-3.24	0.84	-3.84
STAM	ENSG00000136738	-1.53	0.40	-3.84
LOXL3	ENSG00000115318	-3.45	0.90	-3.84
TXNRD1	ENSG00000198431	-2.74	0.72	-3.83

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SPIRE1	ENSG00000134278	-1.74	0.46	-3.81
NAP1L4P1	ENSG00000177173	-1.98	0.52	-3.81
QSOX1	ENSG00000116260	-2.55	0.67	-3.81
CD109	ENSG00000156535	-5.43	1.43	-3.81
MTHFD2	ENSG00000065911	-2.71	0.71	-3.80
DGKA	ENSG00000065357	-1.04	0.27	-3.80
GNAI1	ENSG00000127955	-2.50	0.66	-3.79
DOK1	ENSG00000115325	-1.23	0.33	-3.78
ASNS	ENSG00000070669	-2.17	0.58	-3.77
BAG2	ENSG00000112208	-3.30	0.87	-3.77
LNPEP	ENSG00000113441	-3.24	0.86	-3.77
SERAC1	ENSG00000122335	-1.80	0.48	-3.77
RP11-448G15.3	ENSG00000261490	-2.53	0.67	-3.76
SLC4A2	ENSG00000164889	-1.48	0.40	-3.74
MYADM	ENSG00000179820	-3.35	0.90	-3.72
CYP26B1	ENSG00000003137	-5.46	1.47	-3.72
VPS13A	ENSG00000197969	-2.97	0.80	-3.71
LOXL1-AS1	ENSG00000261801	-2.69	0.72	-3.71
MAP3K9	ENSG00000006432	-3.15	0.85	-3.71
SRD5A1	ENSG00000145545	-2.40	0.65	-3.70
MLF1	ENSG00000178053	-1.86	0.50	-3.70
SEC24D	ENSG00000150961	-1.73	0.47	-3.69
HCN2	ENSG00000099822	-4.59	1.24	-3.69
DGKH	ENSG00000102780	-4.83	1.31	-3.69
ERBB3	ENSG00000065361	-5.61	1.52	-3.68
ZC3H7B	ENSG00000100403	-1.42	0.38	-3.68
AC010761.8	ENSG00000264577	-9.13	2.48	-3.68
IARS	ENSG00000196305	-1.62	0.44	-3.68
FSTL1	ENSG00000163430	-1.54	0.42	-3.68
MMP1	ENSG00000196611	-10.19	2.77	-3.68
COL4A5	ENSG00000188153	-3.07	0.84	-3.66
PTPRK	ENSG00000152894	-3.82	1.05	-3.66
AKIRIN1	ENSG00000174574	-1.23	0.34	-3.65
SCARA3	ENSG00000168077	-2.48	0.68	-3.65
ADAMTS14	ENSG00000138316	-5.34	1.47	-3.64
REV3L	ENSG00000009413	-1.84	0.51	-3.63
LHX4	ENSG00000121454	-7.93	2.18	-3.63
CTTNBP2NL	ENSG00000143079	-2.10	0.58	-3.62
WNT2B	ENSG00000134245	-3.43	0.95	-3.62
DST	ENSG00000151914	-2.02	0.56	-3.62
COL1A1	ENSG00000108821	-2.54	0.70	-3.62
PVRL3	ENSG00000177707	-2.36	0.65	-3.61
AC013470.6	ENSG00000236048	-1.80	0.50	-3.61
SYNJ2	ENSG00000078269	-2.63	0.73	-3.61
TBC1D19	ENSG00000109680	-1.75	0.48	-3.61

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BICD1	ENSG00000151746	-2.38	0.66	-3.60
PPT2	ENSG00000221988	-1.28	0.36	-3.59
MAP4	ENSG00000047849	-1.36	0.38	-3.59
AC005544.1	ENSG00000214167	-5.65	1.58	-3.59
NDFIP2	ENSG00000102471	-1.53	0.43	-3.59
HSPG2	ENSG00000142798	-1.99	0.56	-3.57
SLC36A1	ENSG00000123643	-2.57	0.72	-3.56
PPP1R12A	ENSG00000058272	-1.01	0.28	-3.56
MICALL1	ENSG00000100139	-2.90	0.82	-3.56
C1orf198	ENSG00000119280	-3.36	0.94	-3.56
GLIS3	ENSG00000107249	-5.96	1.68	-3.56
TP53BP2	ENSG00000143514	-1.06	0.30	-3.56
TCF20	ENSG00000100207	-1.19	0.34	-3.55
ACTN1	ENSG00000072110	-2.41	0.68	-3.54
JOSD1	ENSG00000100221	-1.25	0.35	-3.54
N4BP2	ENSG00000078177	-2.23	0.63	-3.54
AMPH	ENSG00000078053	-3.13	0.89	-3.53
DUSP8	ENSG00000184545	-4.28	1.21	-3.53
ARHGAP29	ENSG00000137962	-2.62	0.74	-3.52
FAM114A1	ENSG00000197712	-1.54	0.44	-3.52
NCOA7	ENSG00000111912	-2.89	0.82	-3.52
TRAM2	ENSG00000065308	-3.02	0.86	-3.51
UBE2HP1	ENSG00000253677	-2.32	0.66	-3.50
AMER1	ENSG00000184675	-1.19	0.34	-3.50
MAFG	ENSG00000197063	-1.50	0.43	-3.50
SLC16A7	ENSG00000118596	-7.62	2.18	-3.49
ACTN4	ENSG00000130402	-2.32	0.67	-3.48
ZFHX4	ENSG00000091656	-4.87	1.40	-3.48
RNF217	ENSG00000146373	-1.72	0.49	-3.48
TUBA1A	ENSG00000167552	-2.26	0.65	-3.47
ABL2	ENSG00000143322	-2.22	0.64	-3.47
SYNJ1	ENSG00000159082	-1.50	0.43	-3.47
PLEKHG4	ENSG00000196155	-2.35	0.68	-3.46
PRR14L	ENSG00000183530	-1.35	0.39	-3.46
RP1-152L7.5	ENSG00000216775	-3.63	1.05	-3.46
ZBED4	ENSG00000100426	-1.50	0.43	-3.46
MAN1A2	ENSG00000198162	-1.73	0.50	-3.46
COMT	ENSG00000093010	-1.34	0.39	-3.45
KIF5B	ENSG00000170759	-1.65	0.48	-3.45
LASP1	ENSG00000002834	-1.63	0.47	-3.45
RBM15	ENSG00000162775	-1.55	0.45	-3.44
SLC17A5	ENSG00000119899	-1.59	0.46	-3.43
PLS3	ENSG00000102024	-2.90	0.84	-3.43
PTGS2	ENSG00000073756	-6.34	1.85	-3.43
GFPT1	ENSG00000198380	-1.37	0.40	-3.42

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DBN1	ENSG00000113758	-1.38	0.40	-3.42
SLC5A3	ENSG00000198743	-3.39	0.99	-3.42
XPO6	ENSG00000169180	-1.05	0.31	-3.41
WDR1	ENSG00000071127	-2.06	0.60	-3.41
NDEL1	ENSG00000166579	-1.05	0.31	-3.40
AC098614.2	ENSG00000213846	-2.36	0.69	-3.40
ADRB2	ENSG00000169252	-3.62	1.07	-3.40
CDC42EP1	ENSG00000128283	-2.71	0.80	-3.39
TMEM184B	ENSG00000198792	-1.50	0.44	-3.39
NEK7	ENSG00000151414	-2.28	0.67	-3.39
KIAA1586	ENSG00000168116	-1.32	0.39	-3.39
DDA1	ENSG00000130311	-1.10	0.33	-3.38
PCDH10	ENSG00000138650	-9.84	2.91	-3.38
NTN4	ENSG00000074527	-4.11	1.22	-3.38
SLC1A5	ENSG00000105281	-3.40	1.01	-3.38
AHNAK2	ENSG00000185567	-5.03	1.49	-3.37
CSRP2	ENSG00000175183	-2.25	0.67	-3.37
ARSJ	ENSG00000180801	-5.69	1.69	-3.37
RP4-671G15.3	ENSG00000248201	-1.91	0.57	-3.37
STAC	ENSG00000144681	-9.15	2.72	-3.37
LMO7	ENSG00000136153	-3.26	0.97	-3.37
RP11-360F5.3	ENSG00000249685	-3.29	0.98	-3.37
RGS4	ENSG00000117152	-8.02	2.39	-3.36
SLC4A7	ENSG00000033867	-2.72	0.81	-3.36
MTMR2	ENSG00000087053	-1.16	0.35	-3.35
SYT1	ENSG00000067715	-7.77	2.32	-3.35
CAPN5	ENSG00000149260	-2.75	0.82	-3.35
KLF6	ENSG00000067082	-2.48	0.74	-3.35
BDNF	ENSG00000176697	-9.97	2.98	-3.35
NEK10	ENSG00000163491	-3.77	1.13	-3.34
LOC124685	ENSG00000228118	-2.24	0.67	-3.34
THOC5	ENSG00000100296	-1.51	0.45	-3.34
PDLIM5	ENSG00000163110	-2.36	0.71	-3.34
TSHZ3	ENSG00000121297	-1.70	0.51	-3.34
COL4A1	ENSG00000187498	-4.03	1.21	-3.34
IPO5	ENSG00000065150	-1.63	0.49	-3.34
EPRS	ENSG00000136628	-1.64	0.49	-3.33
GS1-44D20.1	ENSG00000254332	-2.66	0.80	-3.33
COL5A2	ENSG00000204262	-2.81	0.84	-3.32
FAM132B	ENSG00000178752	-6.88	2.07	-3.32
CTIF	ENSG00000134030	-1.56	0.47	-3.32
TUFT1	ENSG00000143367	-3.19	0.96	-3.32
C22orf29	ENSG00000215012	-1.84	0.56	-3.31
PITPNB	ENSG00000180957	-1.73	0.52	-3.31
RICTOR	ENSG00000164327	-1.24	0.38	-3.29

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MICAL3	ENSG00000243156	-1.77	0.54	-3.29
RIMS1	ENSG00000079841	-7.90	2.41	-3.29
RP11-333E13.2	ENSG00000250568	-1.70	0.52	-3.28
TEAD1	ENSG00000187079	-1.36	0.42	-3.28
TFAP2A	ENSG00000137203	-5.43	1.65	-3.28
PPRC1	ENSG00000148840	-1.36	0.41	-3.28
ASB1	ENSG00000065802	-1.57	0.48	-3.28
ACTG1	ENSG00000184009	-1.52	0.46	-3.28
COL4A2	ENSG00000134871	-3.77	1.15	-3.28
LIMS1	ENSG00000169756	-1.64	0.50	-3.27
RP11-145M9.3	ENSG00000181260	-3.15	0.97	-3.27
PGM2L1	ENSG00000165434	-2.47	0.76	-3.26
AL021977.1	ENSG00000256873	-1.58	0.49	-3.26
DUSP5	ENSG00000138166	-5.06	1.56	-3.26
SGIP1	ENSG00000118473	-4.03	1.24	-3.25
TRIB1	ENSG00000173334	-4.13	1.28	-3.24
CYP51A1	ENSG00000001630	-1.41	0.43	-3.24
VPS13B	ENSG00000132549	-1.31	0.41	-3.23
IGF2BP3	ENSG00000136231	-6.94	2.15	-3.23
MYL12A	ENSG00000101608	-1.63	0.51	-3.22
LRRD1	ENSG00000240720	-1.39	0.43	-3.22
INHBA	ENSG00000122641	-5.24	1.63	-3.21
CSRP1	ENSG00000159176	-1.51	0.47	-3.21
PGRMC2	ENSG00000164040	-1.19	0.37	-3.20
MSNP1	ENSG00000251593	-1.55	0.48	-3.20
USP13	ENSG00000058056	-2.21	0.69	-3.20
TPM1	ENSG00000140416	-2.17	0.68	-3.20
DHRS9	ENSG00000073737	-5.47	1.71	-3.20
EDIL3	ENSG00000164176	-7.27	2.28	-3.19
TERT	ENSG00000164362	-10.58	3.32	-3.18
GPRC5A	ENSG00000013588	-6.20	1.95	-3.18
ODC1	ENSG00000115758	-1.78	0.56	-3.18
EPHA5	ENSG00000145242	-11.75	3.70	-3.18
ZNF469	ENSG00000225614	-2.66	0.84	-3.17
ENTPD7	ENSG00000198018	-2.27	0.72	-3.17
FMR1	ENSG00000102081	-1.07	0.34	-3.17
PDLIM3	ENSG00000154553	-4.23	1.33	-3.17
DPY19L1	ENSG00000173852	-1.26	0.40	-3.17
TCF7	ENSG00000081059	-3.26	1.03	-3.17
CTD-3252C9.4	ENSG00000267519	-3.25	1.03	-3.16
PALLD	ENSG00000129116	-3.51	1.11	-3.16
KCNH1	ENSG00000143473	-6.21	1.96	-3.16
OSR2	ENSG00000164920	-8.36	2.65	-3.16
AVEN	ENSG00000169857	-1.54	0.49	-3.16
ADAMTS8	ENSG00000134917	-7.68	2.43	-3.16

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TUBA4A	ENSG00000127824	-3.25	1.03	-3.16
RBMS2	ENSG00000076067	-1.21	0.38	-3.16
DSEL	ENSG00000171451	-1.77	0.56	-3.15
CSGALNACT2	ENSG00000169826	-1.16	0.37	-3.15